

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 14, 2006, 03:55:44 ; Search time 312 Seconds

(without alignments)
2217.666 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQPARARTRTKLFTHRSSV.....QKLISEDLNMTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3665	92.9	6995	2	Q96RK2_HUMAN	Q96RK2 homo sapien
2	3649	92.5	22152	2	Q8WY77_HUMAN	Q8WY77 homo sapien
3	3642	92.3	1148	2	Q9H7S7_HUMAN	Q9H7S7 homo sapien
4	1562.5	39.6	867	2	Q6ZQW5_HUMAN	Q6ZQW5 homo sapien
5	736.5	18.7	258	2	Q9DIH1_MOUSE	Q9DIH1 mus musculus
6	144.5	3.7	1408	2	Q27557_MOUSE	Q27557 methanobact
7	143.5	3.6	656	2	Q7R3P3_GIALA	Q7R3P3 giardia lam
8	141.5	3.6	5010	2	Q4MT18_BACCE	Q4MT18 bacillus ce
9	138	3.5	3443	2	Q8J2M8_MOUSE	Q8J2M8 mus musculus
10	136	3.4	605	2	Q94K06_ARATH	Q94K06 arabidopsis
11	135.5	3.4	1117	1	ENG1_YEAST	ENG1 mus musculus
12	134.5	3.4	1526	2	Q6BLB8_DEBHA	Q6BLB8 debaryomyce
13	132.5	3.4	797	2	Q54E23_DICDI	Q54E23 dictyosteli
14	132.5	3.4	4981	2	Q2PZL6_MOUSE	Q2PZL6 mus musculus
15	131	3.3	1230	2	Q54E54_DICDI	Q54E54 dictyosteli
16	131	3.3	1447	2	Q54UR7_DICDI	Q54UR7 dictyosteli
17	128	3.2	879	2	Q4J6T1_SULAC	Q4J6T1 sulfolobus
18	128	3.2	5017	2	Q81FJ0_BACCR	Q81FJ0 bacillus ce
19	127.5	3.2	1011	2	Q2M1P3_HUMAN	Q2M1P3 homo sapien
20	127	3.2	1166	2	Q4UDM4_THERAN	Q4UDM4 thelaria a
21	127	3.2	1364	2	Q86AL8_DICDI	Q86AL8 dictyosteli
22	126.5	3.2	885	2	Q54V40_DICDI	Q54V40 dictyosteli
23	126.5	3.2	2340	2	Q8U2Z7_9HERP	Q8U2Z7 cat moraic
24	126	3.2	1056	2	Q4VWP3_9HERP	Q4VWP3 tortoise he
25	126	3.2	1818	2	Q54HY5_DICDI	Q54HY5 dictyosteli
26	125.5	3.2	1011	2	Q54HY5_DICDI	Q54HY5 dictyosteli
27	125.5	3.2	1011	2	Q54HY5_DICDI	Q54HY5 dictyosteli
28	125	3.2	1084	2	Q81SK0_BACAN	Q81SK0 bacillus an
29	125	3.2	1084	2	Q8EUS5_MYCPE	Q8EUS5 mycoplasma
30	125	3.2	10791	2	Q7U7M8_SYNXP	Q7U7M8 giardia lam
31	124.5	3.2	1012	2	Q6FQ05_CANCA	Q6FQ05 candida gla

ALIGNMENTS

RESULT 1	ID	Q96RK2_HUMAN	PRELIMINARY	PRT	6995 AA.
AC	Q96RK2				
DT	01-DEC-2001				Integrated into UniProtKB/TrEMBL.
DT	01-MAR-2004				sequence version 2.
DT	07-FEB-2006				entry version 13.
DE	Mucin 16 (Fragment).				
GN	Name=MUC16;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homidae;				
OC	Homo				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NCBIOTIDE SEQUENCE.				
RX	MEDLINE=21347965; PubMed=11369781; DOI=10.1074/jbc.M103554200;				
RA	Yin B.W., Lloyd K.O.;				
RT	"Molecular cloning of the cal25 ovarian cancer antigen. identification.				
RT	as a new mucin, mucin 16."				
RT	J. Biol. Chem. 276:27371-27375 (2001).				
RN	[2]				
RP	NCBIOTIDE SEQUENCE.				
RL	Lloyd K.O., Yin B.W.T.;				
RU	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
CC	Copyrighted under the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NonDerivs License				
CC	EMBL: AF361486; AAK74120.3; -, mRNA.				
DR	HSSP; Q9DIH1; 11VZ.				
DR	SMR; Q96RK2; 6803-6922.				
DR	InterPro; IPR00194; ATPase_a/bcentre.				
DR	InterPro; IPR000082; SEA.				
DR	Pfam; PF01390; SEA; 20.				
DR	SMART; SM00200; SEA; 1.				
DR	PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.				
DR	PROSITE; PS50024; SEA; 6.				
FT	NON TER				
FT	SEQUENCE 6995 AA; 744966 MW; 80C797DDBDF33A2B CRC64;				
QY	Query Match	92.9%;	Score 3665;	DB 2;	Length 6995;
QY	Best Local Similarity	99.9%;	Pred. No. 8.3e-238;		
QY	Matches 696;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	14	FTHRSSVSTSTSTPTGPTVYVIGASKTPTASIFGPEASASHLILFTLNTFTITLRLYEENMPG 73			
QY	6240	FTHRSSVSTSTSTPTGPTVYVIGASKTPTASIFGPEASASHLILFTLNTFTITLRLYEENMPG 6299			
QY	74	SRKFNTERVYLOGLAPLPRKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTRPPTGP 133			
QY	6300	SRKFNTERVYLOGLAPLPRKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTRPPTGP 6359			
QY	134	GDREGLVLESLQTLHSITELGPTLDRDRLVNGFTHRSSVPTSTGVVSEEPFTLNT 193			

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Db      6360 GIDRQLVLELSQLTSHSITELGPPYTLDRDSLTVNGFTHRSVPPTSTGVSEEPFLNFT 6419
Qy      194  INNLRVYADMGQPGSLKFNITDNVAKHLSPFORSSLGARTGCRVIALSVKNGAETR 253
Db      6420  INNLRVYADMGQPGSLKFNITDNVAKHLSPFORSSLGARTGCRVIALSVKNGAETR 6479
Qy      254  VLLCTCYLQPLSGPGLPIKQVFEHLSQOHTGITRLGPRVSLDQSLYNGYEPGDEPPT 313
Db      6480  VLLCTCYLQPLSGPGLPIKQVFEHLSQOHTGITRLGPRVSLDQSLYNGYEPGDEPPT 6539
Qy      314  TRKPATFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLR 373
Db      6540  TRKPATFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLR 6599
Qy      374  PLFQSSMGPPFLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIQOLYWELSQLT 433
Db      6600  PLFQSSMGPPFLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIQOLYWELSQLT 6659
Qy      434  GVTOLGPFYVLDRLDSLFINGYAPONLSIRGEYOINFIHVMNLSNPDPTSEYITLLRDIQ 493
Db      6660  GVTOLGPFYVLDRLDSLFINGYAPONLSIRGEYOINFIHVMNLSNPDPTSEYITLLRDIQ 6719
Qy      494  DKVTTLKGSQSLHDFRFLVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 553
Db      6720  DKVTTLKGSQSLHDFRFLVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 6779
Qy      554  WIGSTYQVLDIHYTEMESVYOPTSSSTOHFYLNFTITNLPYSDKAOPGTTNQRNR 613
Db      6780  WIGSTYQVLDIHYTEMESVYOPTSSSTOHFYLNFTITNLPYSDKAOPGTTNQRNR 6839
Qy      614  NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVSLCNFSLARRVDAIYEEF 673
Db      6840  NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVSLCNFSLARRVDAIYEEF 6899
Qy      674  LRMTNGTOLQNFITLDRSSVLDGYSPPNRNEPLTGN 710
Db      6900  LRMTNGTOLQNFITLDRSSVLDGYSPPNRNEPLTGN 6936

RESULT 2
O8WX17_HUMAN PRELIMINARY; PRT; 22152 AA.
ID O8WX17_HUMAN
AC O8WX17
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 16.
DE Ovarian cancer related tumor marker CA125.
GN Name=MUC16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21646939; PubMed=11786729; DOI=10.1159/000050638;
RA O'Brien T.J., Beard J.B., Underwood L.J., Dennis R.A., Santin A.D.,
RA York L.;
RT "The CA 125 gene: an extracellular superstructure dominated by repeat
RT sequences."
RN Tumour Biol. 22:348-366(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA O'Brien T.J., Underwood L.J., Beard J.B.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AF144442; AL65133.2; -; mRNA.
DR SMR; O8WX17; 21960-22079.
DR Ensembl; ENSG00000181143; Homo sapiens.

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DR HGNC; HGNC:15582; MUC16.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 51.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00152; ATPase_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS50024; SEA; 11.
SQ SEQUENCE 22152 AA; 2353428 MW; B3E7BDP19997A440 CRC64;

Query Match 92.5%; Score 3649; DB 2; Length 22152;
Best Local Similarity 99.7%; Fred. No. 5.7e-236;
Matches 695; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14  FTHRSVSTSTPGPTVYLKASKTPASIFGPSASHLLIFLTNFTITNLYSEBNMPG 73
Db      21397 FTHRSVSTSTPGPTVYLKASKTPASIFGPSASHLLIFLTNFTITNLYSEBNMPG 21456
Qy      74  SRKFVTRVVLQGLRPLFKNTSVGPLYSGRLTLRPEKGEATGVDAICTHRDPGCP 133
Db      21457 SRKFVTRVVLQGLRPLFKNTSVGPLYSGRLTLRPEKGEATGVDAICTHRDPGCP 21516
Qy      134  GIDRQLVLELSQLTSHSITELGPPYTLDRDSLTVNGFTHRSVPPTSTGVSEEPFLNFT 193
Db      21517 GIDRQLVLELSQLTSHSITELGPPYTLDRDSLTVNGFTHRSVPPTSTGVSEEPFLNFT 21576
Qy      194  INNLRVYADMGQPGSLKFNITDNVAKHLSPFORSSLGARTGCRVIALSVKNGAETR 253
Db      21577 INNLRVYADMGQPGSLKFNITDNVAKHLSPFORSSLGARTGCRVIALSVKNGAETR 21636
Qy      254  VLLCTCYLQPLSGPGLPIKQVFEHLSQOHTGITRLGPRVSLDQSLYNGYEPGDEPPT 313
Db      21637 VLLCTCYLQPLSGPGLPIKQVFEHLSQOHTGITRLGPRVSLDQSLYNGYEPGDEPPT 21696
Qy      314  TRKPATFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLR 373
Db      21697 TRKPATFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLR 21756
Qy      374  PLFQSSMGPPFLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIQOLYWELSQLT 433
Db      21757 PLFQSSMGPPFLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIQOLYWELSQLT 21816
Qy      434  GVTOLGPFYVLDRLDSLFINGYAPONLSIRGEYOINFIHVMNLSNPDPTSEYITLLRDIQ 493
Db      21817 GVTOLGPFYVLDRLDSLFINGYAPONLSIRGEYOINFIHVMNLSNPDPTSEYITLLRDIQ 21876
Qy      494  DKVTTLKGSQSLHDFRFLVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 553
Db      21877 DKVTTLKGSQSLHDFRFLVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 21936
Qy      554  WIGSTYQVLDIHYTEMESVYOPTSSSTOHFYLNFTITNLPYSDKAOPGTTNQRNR 613
Db      21937 WIGSTYQVLDIHYTEMESVYOPTSSSTOHFYLNFTITNLPYSDKAOPGTTNQRNR 21996
Qy      614  NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVSLCNFSLARRVDAIYEEF 673
Db      21997 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVSLCNFSLARRVDAIYEEF 22056
Qy      674  LRMTNGTOLQNFITLDRSSVLDGYSPPNRNEPLTGN 710
Db      22057 LRMTNGTOLQNFITLDRSSVLDGYSPPNRNEPLTGN 22093

RESULT 3
O9H7S7_HUMAN PRELIMINARY; PRT; 1148 AA.
ID O9H7S7_HUMAN
AC O9H7S7
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 19.
DR CDNA FL114503 F18; Clone PLACE2000132.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

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OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Makamatsu A., Hayashi M., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Odayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiraori A.,
Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y.,
Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
Oono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
Togiyama S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
Mashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shichata N., Sano S.,
Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Okamoto S.,
Kawabata A., Hakihi T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Maehuo Y., Yamashita R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs";
RL Nat. Genet. 36:40-45(2004).
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CC
DR EMBL: AK024365; BAB14899.1; -; mRNA.
DR HSSP: Q9DIH1; IIVZ.
DR SMR: Q9H7S7; 956-1075.
DR InterPro: IPR000082; SEA.
DR Pfam: PF01390; SEA: 7.
DR PROSITE: PS50024; SEA: 3.
SQ SEQUENCE 1148 AA; 127958 MW; 3861B0D5FED8A8C CRC64;
Query Match 92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 2e-237;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 14 FTHRSSVSTSTGCTPTVYVYGAKTPTASIFGSAASHLLTLFTLNTTNTLRKEMWPG 73
393 FTHRSSVSTSTGCTPTVYVYGAKTPTASIFGSAASHLLTLFTLNTTNTLRKEMWPG 452
74 SRKFTTERVLOGLRLPLFKNTSVGPYSGRLLTLRPEKDGATGDAICTHRPDPG 133
453 SRKFTTERVLOGLRLPLFKNTSVGPYSGRLLTLRPEKDGATGDAICTHRPDPG 512
134 GLDREOLYELSQLTHSITELEGPYLLDRDSLVLVNGFTHRSSVPTTSTGVSEEPFLTNFT 193
513 GLDREOLYELSQLTHSITELEGPYLLDRDSLVLVNGFTHRSSVPTTSTGVSEEPFLTNFT 572
194 INNLRTWADMGQGSLSKENTDVMKHLSPLEFORSISGARVGCYVIALRSYKNAER 253
573 INNLRTWADMGQGSLSKENTDVMKHLSPLEFORSISGARVGCYVIALRSYKNAER 632
254 VDLCTYLPGLSGPLPIKQVPHLSQOTHTGIRLGPYSLDKSLVLYNGNEBGPDEPT 313
633 VDLCTYLPGLSGPLPIKQVPHLSQOTHTGIRLGPYSLDKSLVLYNGNEBGPDEPT 692

QY 314 TPKPATFLPLPSEATTAMGYHLKTLTLNFTTISNLQYSPDMKSGASTNTEGVLOHLR 373
DB 693 TPKPATFLPLPSEATTAMGYHLKTLTLNFTTISNLQYSPDMKSGASTNTEGVLOHLR 752
QY 374 PLFQKSMGPPFLYGQOLISLREPKDGAATGVTCTYHPDPVPGIDIQOLYWEISQLTH 433
DB 753 PLFQKSMGPPFLYGQOLISLREPKDGAATGVTCTYHPDPVPGIDIQOLYWEISQLTH 812
QY 434 GTTQGLFYLLDSDSLFINGYAPQNLSTIGEYQINHIYMNLSNDPPTSEYITLLRDQ 493
DB 813 GTTQGLFYLLDSDSLFINGYAPQNLSTIGEYQINHIYMNLSNDPPTSEYITLLRDQ 872
QY 494 DVTTLTKGSGQADHFRFLCVTLNLTMDSVLTVKALFSSNDPSPVEQVFLDKTNASPH 553
DB 873 DVTTLTKGSGQADHFRFLCVTLNLTMDSVLTVKALFSSNDPSPVEQVFLDKTNASPH 932
QY 554 WLGSTYQVLVDIHVTMESSVYQPTSSSTQHFYLNFTTNLPYSQDKAQPGTTYNQRK 613
DB 933 WLGSTYQVLVDIHVTMESSVYQPTSSSTQHFYLNFTTNLPYSQDKAQPGTTYNQRK 992
QY 614 NIEDALNQLFRNSSIKYFSDCVSTFNSVPRHHTGVDSLCSNPPLARVDVAIYEEF 673
DB 993 NIEDALNQLFRNSSIKYFSDCVSTFNSVPRHHTGVDSLCSNPPLARVDVAIYEEF 1052
QY 674 LMTNNGTQLONFLDRSSVLVDGYSPNRPBPLTGN 710
DB 1053 LMTNNGTQLONFLDRSSVLVDGYSPNRPBPLTGN 1089
RESULT 4
Q6ZOW5 HUMAN PRELIMINARY; PRT; 867 AA.
ID Q6ZOW5;
AC Q6ZOW5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE CDNA FLJ46845 fig. clone UTRU3001946, highly similar to Homo sapiens
mucin 16 (MUC16).
DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Uterus;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shichata N.,
Matsumura K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
Matsumura Y., Moriya S., Chiba B., Momiyama H., Onogawa S.,
Kaeriyama S., Satoh N., Matsunawa H., Takahashi B., Katakawa R.,
Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Makamatsu A.,
Ishii S., Yamamoto J., Isono Y., Kawai-Hiro Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kikuchi H., Kanda K., Magatsuna M., Murakawa K., Kanehori K.,
Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Maehuo Y., Nagai K., Isogai T.;
RT "NEO human cDNA sequencing project";
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
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CC
DR EMBL: AK128681; BAC87568.1; -; mRNA.
DR InterPro: IPR000082; SEA.
DR Pfam: PF01390; SEA: 4.
DR PROSITE: PS50024; SEA: 2.
SQ SEQUENCE 867 AA; 96201 MW; C7B3033258839622 CRC64;
Query Match 39.6%; Score 1562.5; DB 2; Length 867;
Best Local Similarity 46.3%; Pred. No. 9.9e-97;
Matches 356; Conservative 102; Mismatches 234; Indels 77; Gaps 17;

QY	14	PHRSSVSTSTSPGPPVTYVLGASKTPASIFG8BAASHLL1FLTNFTITNLRYEENM-WP	72
Db	101	FTHRNFVPTTSPGISTVH1G7SETPSSLPRIVPGLVLPFTLNFTITNLQYEAMRH	160
QY	73	GSRKNTTTRVVLQGLRLPFKNTSVGPIVSGGCTLLRPEKDEAVGDAICTHRDPPTG	132
Db	161	GSRKNTTTRVVLQGLRLPFKNTSTIGPIVSSCCTLLRPEKDXAARVDAICTHHDDPS	220
QY	133	PGIDREOLVLELSQLTHTSITELGAPYLLDRDSLVYNGFTHRSSVPTST	180
Db	221	PGANREOLVWELSQLTHGITELGAPYLLDRHSLVYNGFTHQSSWTTTRTPDTSIMHLATSR	280
QY	181	-----GVSEEP-----FTLNFTINLRYAMDMGCGSLKFNITDVMGHLSPLFQRS	230
Db	281	TPASISGPTTAAPRLVLPFTINFTITNLRYEENMHGSRKNTTTRVLQGLRLPFKNTS	340
QY	231	IGARTYGCVIALRSVYNGAETFDVLCYLOPLSGPGLPIKQVFNHLSQOTGIRLGP	290
Db	341	VAPLYSGCLTLLRPFKQDAATVDAICTHRPDKPGIDREOLVWELSQLTHSITELGP	400
QY	291	YSLDKDSLVLNGYNEBPDPEPTTPKAT-----TFLPPLSE-ATTAMGHLKTLTLNF	343
Db	401	YTLDRDSLVLNGPQTQ--RSVPTTSTIGPPTVDLGTSGFVSKPGPSAASPLVLFTLNF	458
QY	344	TTSNLTQSPDM-GKGSATNSTSTEGVQLHLRLPFQKSSMGPFLGCOLSLRPEKQGAAT	402
Db	459	TITNLRYEENMHGPGSRKNTTTRVVLQGLRLSPKSTSVGPIVSGGCTLLRPEKQGTAT	518
QY	403	GVDTTCTYHPDPGPGILDLOQLVWELSQLTHGVTOLGPFYLLDRDSLPFINGAPON-----	457
Db	519	GVDALCTHHPDKSPRLDRBOLVWELSQLTHNITELGAPVALDNDLSLFVNGFTHRSSVSTT	578
QY	458	-----LSIRGE-----YQINPHIVMNL-SNPDPFSSEYITLLRD	491
Db	579	STPGPTPVVLGASKTPASIFG8BAASHLL1FLTNFTITNLRYEENMHGSRKNTTTRV	638
QY	492	IDDKVTTYKGSQLDHTRFCLVTNL--TMDSVLVTVKALFSSNLDRSLV---EQVFLD	545
Db	639	LOGGLRLPFKNTSVGPIVSGGCTLLRPEKQGAATVDAICTHRPPTGGLDRBOLYLE	698
QY	546	-KTINASFWLGS-TYQVLDIHTEMESSYQPTSSS---STGHFVLPFTITNLPLYSQDK	600
Db	699	LSQLTHTSITELGAPYLLDRDSLVYNGFTHRSSVPTTSTGVSEEPFTLNFTITNLRYADM	758
QY	601	AOPGTTNYORKNKINIDALNQLFRNSSIKSPFSDQVSTFRSVPNRHGTVDSLGNF-SP	659
Db	759	GQPGSLKFNITDVMGHLSPLFQRSLSGARYGCVIALRSYNGAETFDVLCYLOP	818
QY	660	LA-RVDRVAIYEEFLMTRNGTOLONFTLDRESSVLVDGYSFNNRNEPLT	707
Db	819	LSGPGCLPIKQVFNHLSQOTHTGIRLGLPYSIDKDSLVLNGHTTLQROSTT	867
RESULT 5			
Q9DIH1_MOUSE			
ID	Q9DIH1_MOUSE	PRELIMINARY; PRT; 258 AA.	
AC	Q9DIH1;		
DT	01-JUN-2001,	integrated into UniProtKB/TrEMBL.	
DT	01-JUN-2001,	sequence version 1.	
DT	07-FEB-2006,	entry version 22.	
DE	18-day embryo whole body cDNA, RIKEN full-length enriched library,		
DE	clone:1110008114 product:hypothetical SEA domain containing protein,		
DE	full insert sequence.		
GN	Name=1110008114Rik;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	NCBI_EOTIDE_SEQUENCE.		
RP	TISSUE=Whole body; PUBMED=C57BL/6J;		
RC	MEDLINE=99279253; PubMed=10396636; DOI=10.1016/S0076-6879(99)03004-9;		

RA Carninci P., Hayashizaki Y.:
RT "High-efficiency full-length cDNA cloning.",
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RN
RA Carninci P., Kankawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard A., Wells C., Kodias R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmring L.G., Adkins J., Allen J.B.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Banerl M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Cluttbuck D.R.,
RA Chow M.L., Dalla S., Dalrymple B.P., de Bono B., Della Gatta G.,
RA Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Fukui S., Gariboldi M.,
RA Georgakilas G., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayesashi Y., Henrich T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jatk M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Larreau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Lunni S., McWilliam S., Madan Babu M., Medzera M., Marchionni L.,
RA Matsuda H., Matczuska S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottegull-Traber S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Peasele G.,
RA Petrovsky N., Piazza S., Reed U., Reid J.F., Ring B.Z., Ringwald M.,
RA Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schombach C., Sekisuchi K., Semple C.A., Sengo S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupp E., Sugitara K., Sultana R., Takenaka Y., Teki K.,
RA Tamomoja K., Tan S.L., Tang S., Taylor M.S., Tenen J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen B., Verardo R., Wei C.L., Yeaghi K.,
RA Yamamichi H., Zbarovsky E., Zhu S., Zimmer A., Hide W., Bull C.,
RA Grummond S.M., Teasdale R.D., Liu E.T., Brucic V., Quackenbush J.,
RA Walstedt C., Mattick J.S., Hume D.A., Kai C., Saeki D., Tomaru Y.,
RA Futaba S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida Y., Imanura K., Itom M., Kato T., Kawaji H., Kawagashita N.,
RA Kawashima T., Kojima K., Kondo S., Konno H., Nakano K., Niimomiya N.,
RA Nienho T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanishi A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.:
RT "The transcriptional landscape of the mammalian genome.",
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG ("Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.",
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RN
RA Okazaki Y., Furuno M., Kankawa T., Aochi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Bachdallil R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,
RA Schindler L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Choibha C., Corbani L.E., Cousins S.,
RA Dalla E., Draganti T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gallateland T., Gariboldi M., Glasi C., Godzik A., Gough J.,
RA Girimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Karai A., Kawasaki H., Kawasawa Y., Kedziński R.M., King B.L.,
RA Kagawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.U., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid U., Ring B.Z., Ringwald M.,

RA Sandelli A., Schneider C., Sempke C.A., Seiou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vetraro R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Boris A., Yamagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shitaki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sasaki K., Sasaki D., Shibata K., Shingagawa A.,
RA Yaunushli A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y. ;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs." ;
RL Nature 420:563-573(2002).
[5]
NN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=21085566; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia A.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sasaki K., Okido T., Furuno M., Aono H., Baladrelli R., Bersh G.,
RA Blake Y., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Ralstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guertinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Maibach M., Mazzarelli U., Monteberti N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitteker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection." ;
RL Nature 409:685-690(2001).
[6]
NN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
RX Carninci P., Shibata Y., Hayatsu M., Sugihara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y. ;
RT "Normalisation and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes." ;
RL Genome Res. 10:1617-1630(2000).
[7]
NN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=20530913; PubMed=11078651; DOI=10.1101/9r.152600;
RX Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kusunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer." ;
RL Genome Res. 10:1757-1771(2000).
[8]
NN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arikawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hizumoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sasaki C., Sasaki K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingagawa A., Shitaki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

[illegible]

DR Pfam; PF06739; SBBP; 7.
 KW Complete proteome.
 SQ SEQUENCE 1408 AA; 152737 MW; 294EC742ABB29F2 CRC64;
 Query Match 3.7%; Score 144.5; DB 2; Length 1408;
 Best Local Similarity 20.1%; Pred. No. 2.4;
 Matches 157; Conservative 99; Mismatches 258; Indels 269; Gaps 40;
 58 NRTIINLRKEENMMPSRRKPTNT---ERTLOGLRLPFRKTSVGPRLYSCTRLTLRPRD 114
 444 NRTVLT---PACRKNLTGSDGFLTRPTTISNISVTP--- 480
 115 GRATGVDAICTHRPPTGPGDLREBOYLRL-SQLTSHITELGPLYTLDRSLVYNGTHRS 173
 481 ---NOTGP---LTVTLRGNINTCGDSGTWRD---LVING--RT 515
 174 SVPTSTGVSSBEPPTINFTI-----NLRVWADMQ 205
 516 AGKWEVSGLETEPEFEFEYTLNNSRAYSVGVNPPATRVFLGPLIPENLRVTPSGQ 575
 206 PGLKKNITDNWKKHLSPLFORSSLGARYTGCRIALASVNGAETRY----- 254
 576 E-PLKVNVTADLVNVDLPDSTYAEI---YIDGVLLDSNVTVNASSRTTTSFNRTLAAG 631
 255 --DLCTVLP---LSGPGLEPIKOVFHELSQOTHG-----ITRL--GPYSIDK 295
 632 LVEITINDLEPELVYVMEGRKFIEN--FTLTPGSGAALVTYVSAMITNIDSNPSTYA 689
 296 DSLYLNG-----YNEPGDEPPTPKPATYFLPLSBAATTAMGVH---LKTTL-LNF 343
 690 -TIYVGVGDHTKVLNIPGSS--TVPFSTSLIPRGVLTISLNNNVSGTVRVLSEANF 745
 344 TISNLOVSPDMGSGATFSTBGLHLRLPLFKSKMCPFYIGCOLISLRPKQGAANG 403
 746 TISNVTVSPVSGKSPINVTVAIV-----RNNGDLAG 777
 404 VPTCTYHPDPVPGGLDIQOLYWEISQLTHGVTLQFVYLDRLDRLFLNGVAPONLSIRGE 463
 778 -DPAVTLYLDVA-----WETRTVS-----VPGKSSVLS--FKKELAFGE 816
 464 YQINFIH---VNMNLSNPPTSSEYITLLRDIDQKVTTLKYSQQLDTRFCL-VTN--- 516
 817 YRLNLSGTDTVIRVLEPDTIRGF-----NVTPLTGPAPL--SVRASLNTVTPND 865
 517 -----LTMSVLYTVKALFSSNIDPSLVEQVFLDKTLNLSFHWLG----- 556
 866 LVIGFTARLMDGVVVOENIV---SLSPETREIANGTLLTPGNHTVVGINBSKIYRVLR 922
 557 -STYOLVDIHTVMESSVYOP-----TSSSSTOHFYLNFT---ITNLPSYODKAQPGT 605
 923 PASITISDLRYT--PSSGSEPLITTATATARKTGEVDGNTTAVLYINGLANVDEKNTVGA 980
 606 TNYQRKNRIEDALNOLFRRNSI-----KSYPSDCQVSTFRSVP---NRHHT 649
 981 -----GRSVQVAFNHTIENAGIYLAGISGLTPLDVRVLSBPASIMLSATPLGVGSPHRI 1034
 650 GVDLSLGNFS-----PLARVRVVAIYEBFLMTANGTOLQNTIDRS-----SVLYNG 697
 1035 IYVALVSTBERGSGNTAGLYDGVNVQNRVTAVTGPVLSVPLADISBGRHQTVAIS 1094
 698 YSP 700
 1095 LSP 1097

RESULT 7
 QTR3F3_GIALA PRELIMINARY; PRT; 656 AA.
 AC QTR3F3;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-FEB-2006, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE GUP_158_79919_77949.

OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
 OC NCBI_TaxID=164922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBS databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBS whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL; AACB0100015; EAA41889.1; -; Genomic DNA.
 DR HSP; P10081; 1PDK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR01545; DEAD/DEAH N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 KW ATP-binding; Helicase; Hydrolyase.
 SQ SEQUENCE 656 AA; 73379 MW; EBF73D219C01978B CRC64;
 Query Match 3.6%; Score 143.5; DB 2; Length 656;
 Best Local Similarity 21.1%; Pred. No. 0.89;
 Matches 114; Conservative 63; Mismatches 185; Indels 179; Gaps 24;
 271 IKQV-----FHELSQTHGIRTLGPGYSLDKSLYLN---GVNEPGDEPPTPKPATF 321
 116 IREVPRIATFEDLSR-----PPDDPE--VQNTYRAKYFQPLPIQKALP----- 160
 322 LPLSEATTAMGYHAKTL-----TLNFTISNLO-----YSPDMG----- 355
 161 -----TGMVGYDILLACQSGSKTCAFIILIRIATEKXKLTWMSGHEDRFRN 213
 356 -KGSATFNSTBGLVHLRLPLFKSKMCPFYIGCOLISLRPKQGAAGVDTCTYHPRP 414
 214 AKGSRAYPC--IIMSPTRRLVQOTAKASWML-----SYGTSILTRVAYGGP 259
 415 VPGGLDIQOLYWEISQLTHG-----VTOLGFVYLDL--DSLFLNGVAPONLSIR 461
 260 SSPQRDALQMGCDILVATFGRLLDPIKQGVETTVRFVFEBCRMIDMGSEFQIRDL 319
 462 GEYQINFIHVNMLSNPPTSSEYITLLRDIDQKVTTLKYSQQLDTRFCLVTNLTM-D 520
 320 HELPRHHSVQ--DPENPDITHQ-----IERQTLFSAATFRE-----IKULAMEF 363
 521 -----SVLTVAKALFSSNIDPSLVEQVFLDKTLNLSFHWLGSTYOLVDIHTBMESSVYQ 575
 364 LRQDRLVSTVQIGSSN--PMLAQRVVLYVERSNKRLRL----- 401
 576 PTSSSTOHFYLNFTITNLPSYODKAQPGTMYQRKNRIEDALNOLFRRNSIKSYPSDC 635
 402 -TEYITGNADANNLIEV-YGTDKEQ-----DPSLSTVSSTAIGISEEFNRA 446
 636 QVSTFRSVNRRHHTGDSL-----CNFSPLARV-----DRVAIYEBFL 674
 447 KNAIY---PDSIAARHDTLANKGIIIOYQITVTFNFRSEADRIFRFEDMKRYVAVIHGM 503
 675 RMTNRGTOQLNFTLDRSSVLYVDGYSNR-----NEPLTGNASADIQSGRSSILE 723
 504 TQKERENNLKYFKAGRTNLTIGTVAQRGLDIPVRLVLYNDLPGNVDDYTRIGTGRA 563

OY 724 G 724
Db 564 G 564

RESULT 8
O4MT18_BACCE PRELIMINARY; PRT; 5010 AA.
ID O4MT18; Q4MT18; 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Cell surface protein.
GN ORFNames=BCE_G9241.620;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_Taxid=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Riltone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AAEK0100008; EAL15315.1; -; Genomic DNA.
CC GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
CC InterPro; IPR000850; Adenylate_kin.
CC InterPro; IPR000194; ATPase_a/Dcentre.
CC InterPro; IPR001434; DUF11.
CC Pfam; PF01345; DUF11; 26.
CC TIGRFAMs; TIGR01451; B_ant_repeat; 35.
CC PROSITE; PS00113; ADENYLATE_KINASE; UNKNOWN_1.
CC PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
CC Repeat.
CC KW
SQ SEQUENCE 5010 AA; 521891 MW; B00914651BF832DD CRC64;

Query Match 3.6%; Score 141.5; DB 2; Length 5010;
Best Local Similarity 18.5%; Pred. No. 26;
Matches 153; Conservative 123; Mismatches 328; Indels 223; Gaps 36;

OY 10 RRLKTHRSVSTTSPGRTFYVGLASKTPASIFGSSASHLLIFLTNFTTNLRKEN 69
Db 3658 QAOULTTKTSNPTVDIGTITLYISEVKIGNV-----DANINILFT-----D 3699
OY 70 WPGSRKFTTERVVOGLLRP--LFKNTSVGLPVSGLRTLL-----RPEKDGATG- 119
Db 3700 SIPAGTTFVPSDVTNGVQOPTNPENGISIGTIPNSKTLIFVQVTNNPTEHEIVNQ 3759
OY 120 VDAICTHRDPTGPGGLR-----EQLYELLSQ--LTHSITEL 154
Db 3760 SSAMVQYVSIPTAPVNRATSNIVTSLQNNNIISIKQADVTFAISQNTFYTWLQNI 3819
OY 155 GGYTLD-----RDSLYVNGFTIRSSNP--TSTGVSESEPTLNTINN 196
Db 3820 GTVPANNLIFDINIPGTFIFEDSISINNVIOGAPNENGITLGTIQPEVTYISFOVL 3879
OY 197 LRYMADMGPGSLKFNITDNVMKHL---SPLFORSSLGARYT---GCRVIALNSVKNG 249
Db 3880 TSI-----PPGNTVINISDTSYEQIEPSPSIIQRSLSNATVTEVRTANVGLASA-NR 3933

OY 250 AETRYDLCTYLOPLSGPG-LPIKOVFHELSQOHTGTRLGPSLDKSLVINGYNEPGP 308
Db 3934 SITRIGQIITTVAVTNAGYPIITWTL--LIDAIAGTTFIPNSILVDGI-----PP 3984
OY 309 DEPTTPKPAATFLPPLSEATATMGYHLKTLT-----NETISNLOYSPP--MGKGA 359
Db 3985 NENPIITGLTNILP--NNITIVFQVNVVSIPONNININAVIHYEQPPSPPISE 4041
OY 360 TPNSTEGVLOHLRLPFOKSSMGPFYLGQ-----LISLRPEKDGAATGDTCTYHP 412
Db 4042 TTSSNTTNIQFDALILITKSKANTLIANIDETIEYTVLI---QNNGSTT---TNSIFPT 4094
OY 413 DPVGRGLDIQQLYWEISQLTHGVQLGFRVYLDKSLFIN-----GYAPQNLSTR 461
Db 4095 DTIEDGA-----VTPGSGVIVNNVYLPADNRIGISIRINIAS 4132
OY 462 GEYQINFHIVMWNLS--NPDPSTSEVI-----TLARDIODKVTTLVYKGSQALHD---TF 509
Db 4133 QATITTFQVSVTNLPAVNPPTNTANIYVDFIENPDPFAPIQKSTSTNTTFVQINDADIVGL 4192
OY 510 RFLCVTNLTMDSVLVTKALFSS-NLDPQLVEQVFLDKTLNASFHVLGSLTYQLVDIHYTE 568
Db 4193 KTVDLTSTVIGIDILTYTTTLANTGNTDATAV--VFETDNI PG-----GTFP-----IDGSV 4240
OY 569 MESSVYQPTSSSTGHFY-----LNFITTNLYSQDKAQPGTTVQRKKNIE 616
Db 4241 LVNNIPQLNAPSTILVGTAPNISIVPESVIVIALPASGHVONOSTRYTIN----- 4295
OY 617 DALNQLFNSSIKSYFSCQVSTFERSVNRHHTGVDSLCNFSPLARVDRAVYVEFLRM 676
Db 4296 -----GEOQISTSNITFEVTITAVTAKTTPi-QYADLQIITTYTISI 4338
OY 677 TRNGT-QLQNFLLD-----RSSVLVDGYSFNRNEPLTNSAD 712
Db 4339 TNNGNIQVENIIVTDIIPANTSFIENSIVYVNGNAPNDNPISGLIQID 4385

RESULT 9
Q8JZM8_MOUSE PRELIMINARY; PRT; 3443 AA.
ID Q8JZM8_MOUSE
AC Q8JZM8; 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE MUC4.
GN Name=Muc4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Svt.
RX MEDLINE=22079426; PubMed=12084055;
RA Desseyn J.-L., Clavier A., Laine A.;
RT "Cloning, chromosomal localization and characterization of the murine
RT mucin gene orthologous to human MUC4."
RL Eur. J. Biochem. 269:3150-3159(2002).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AF441786; AAM66254.1; -; mRNA.
CC EMBL; AF520423; AAM66746.1; JOINED; Genomic DNA.
CC EMBL; ENSMUSG00000035656; Mus musculus.
CC WGI; WGI:2153525; MUC4.
CC GO; GO:0007160; P:cell-matrix adhesion; RCA.
CC InterPro; IPR005533; AMOP.
CC InterPro; IPR006210; EGF_3.
CC InterPro; IPR007442; EGF_3.

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DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR003886; NIDO.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF03782; AMOP; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF06119; NIDO; 1.
DR Pfam: PF00094; VMD; 1.
DR SMART: SM00723; AMOP; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00539; NIDO; 1.
DR SMART: SM00216; VMD; 1.
DR PROSITE: PS00856; AMOP; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS00026; EGF_3; 2.
SQ SEQUENCE 3443 AA; 365216 MW; 86CC32D3226F632B CRC64;

Query Match 3.5%; Score 138; DB 2; Length 3443;
Best Local Similarity 20.8%; Pred. No. 25;
Matches 182; Conservative 92; Mismatches 324; Indels 276; Gaps 40;

QY 16 HRSSTSTSTGTPV-----YLQAS-----KTPASIF-----GPSASHLLIFLINF 59
DB 1391 HTGSMGTSSNPQSTTTPVTTSTLSASSRDQVQTEITSQRTIPPEETTTSHASSLSGSP 1450
QY 60 TITNL--RYEENMMPGSRKFTTERVLOQ-----LLRPLFKRTSV--GPLVSGRLT 107
DB 1451 STTNMLTTSTSTQITSGDTRHTTAIVTQSTPATQTSLTSSQMSVTSAPITSSQLS 1510
QY 108 LLRPBK-----DGEATGDAICTHRPPTGPGDLREQLYLELSQL----- 147
DB 1511 TLRGQHTGSKGTSNHOQTITTPVVTTSPTSAT-----SRDQIQTEITSIRITSPGETTTS 1566
QY 148 -THSTIELGPTTLDDSLVNGFTIRSSVPTTS-----TGVSSE--EPFLINFIN-NL 197
DB 1567 HASSLSSSGSPST-----TNMLTSTSTQITSGDTRHTTAIVTQSTPATQTSLTSS 1619
QY 198 RYMADMGPGSLKFNITDNVMGHLSPFORSSLGARYTGC----- 238
DB 1620 RNMSIVSTP-----ITST--HKSLTLPQROHTSKGTSNPQTTPPEMTTSPATS 1670
QY 239 -----RVIA-----LRSYKNGAETRYDL----- 256
DB 1671 HDLIERETSSQRTISGETTTSYADIMSSASPTTHMLSTSTSTSVDRHTTTLMTQ 1730
QY 257 -----LCYLIQP-----LSGPGLPKQVFBLS---QQT-----GITRLG 289
DB 1731 GSTPATTVQVSPSSKNMSTVSTPTIST-HKSLTLPQSOHTGSKGTSNPQTTPPEVTST 1789
QY 290 PYSLDKDSLNGVNEP--GPDEPTTPKPAFTFLPLSEATTAGYHLKTLTNFTISN 347
DB 1790 PSATTRDQIQTESSQRTISPEETTTSHAFSMSLAP---STTN-----LSTTSS 1838
QY 348 LQYSPDMKGSA--TFNSTEGVLQ-----HLRPLPQKSSMGPFLYG 387
DB 1839 QSTSDTGHTTAIVRQGSTPATTVQSLSSQNTISTVSTMTSTHKLSTLPQSOHTGSM--- 1895
QY 388 COLISLRPEKGAAGVDTTCTYHPDPVPGGLDIQOLYWEISQLTHGYTQLGFLYLDSDS 447
DB 1896 -----GTSNPOQTITL-----P-----EVTTSPTSAT--SYDDIQIET 1926
QY 448 LPIINGAPONTLSIREYOINFIIVMNLNSNDPT-----SEEVTLILRDIQDKYTLTYK 501
DB 1927 SFQRTISP-----GETTTS-HAPMSNSAPESSTHKLSTASTETLTSV-DTRHTTAITTE 1978
QY 502 GSQLDHTRFCLVNTLTMDSV-LVTYKALFFSNNLPSLVEQVFLDKTNLASFHMLGSTYQ 560
DB 1979 GSTTLANT-----QSLTSPSSQMSVTSAPITSSQLSTLRQSOHTGSKGTSNHOQTITTP 2033
QY 561 LVDIVTEMESSVYPTSSSTQHTYLANFTTNLPIYQDKAOPGTTNTQKRNKRIED--- 617
DB 2034 VVTTSTPSATSRDQIQTEITSIRITISPDGTTTSHAASSMSSEPNTHLLITTSSTESTSV 2093

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QY 618 -----ALNOLFRNSSIKSYFSDCCVST-----FRSVPNRHHTGVDLSLNF 658
DB 2094 DTGSHVITTHGSLTATTVQSLTPSSQMSVTSMPSTSSQELTSLPQROHTG--SMETSS 2151
QY 659 PLARRVDRVAIYEEFLMKRTNGTLOLQNFPLDRSS 692
DB 2152 QPONITPTVTTSTLLSFRSGSTELQTMWGTSS 2185

RESULT 10
ID Q94K06 ARATH PRELIMINARY; PRT; 605 AA.
AC Q94K06;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE tRNA adenylyltransferase-like protein.
GN Name=t22j18.17; Ordered locus names=Atlg22660;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OK NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.,
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.,
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the tRNA nucleotidyltransferase/poly(A)
CC polymerase family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative License
CC -----
CC EMBL: AF370489; AAK43866.1; -, mRNA.
CC DR EMBL: BT000361; AAN15680.1; -, mRNA.
CC DR TAIR: Atlg22660; -.
CC DR GO: GO:0005739; C:mitochondrion; IDA.
CC DR InterPro: IPR012277; poly(A).
CC DR InterPro: IPR002646; polyA_pol_reg.
CC DR PANTHER: PTHR13734; PolyA_pol; 1.
CC DR Pfam: PF01743; PolyA_pol; 1.
CC KW Nucleotidyltransferase; RNA-binding; Transferase.
SQ SEQUENCE 605 AA; 68954 MW; 2DB278EA9368A18 CRC64;

Query Match 3.4%; Score 136; DB 2; Length 605;
Best Local Similarity 20.6%; Pred. No. 2.5;
Matches 99; Conservative 67; Mismatches 185; Indels 130; Gaps 20;

QY 113 KDGEATGVDAICTHRPPTGPGDLREQLYLELSQLTHTITELGPTTLDRDLSLVNGFTNR 172
DB 152 RDEEVQG-DVIERNPD-----QSGHETALC-----RIYQWIDFVNLRSSEYEN 197
QY 173 SSVPTSTGVVSEBFTLFTINNLRVYADMGQPGSL-KFNITDNVMGHLSPFORSS- 230
DB 198 SRIPFMKGTAKDAFRDLINSLFYNINGAVEDLTERGIDDKSGKIYTPAPKATF 257
QY 231 -----LGARYTGCVIALRSYKNGAETRYDLCTYLOPLSGPGLPKQVFBEL 278
DB 258 LDDPLRLAVRFGARFGFTLDEELKEAASSBEYVAL-----GKISRIRIGNEI 308

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QY 279 SQQTHG-----ITRLGPYSLDKSLYNGVNEGPDEP-----PTTKP 317
 Db 309 DLMISGNBPVSAVITLSDIKLFSVVPALPSSAEPSPENCGLSOSYLEAMSLIKTTPP 368
 QY 318 -----ATTFLP-----PLSEATTANGYHLK 337
 Db 369 GKFSGEQRALYALMFLPFRKTVKDKGKIPVNHIFKFSMRKTSDAETVNHQIT 428
 QY 338 TLTNFTISNLQYSPDMGKSGATFNSREGVLCH-----LLRLPLFKSGMGPYILCCOLIS 392
 Db 429 TERFSLPLSPLEVKDKDELDTW--AADILEHMKSTILNDEIVATSKIRVLGT--FL 483
 QY 393 LRPEPD-----GAATGVDTTCYHPDPVGGGLDIQOLYMELSQL--THGTQLGPFVLDLD 446
 Db 484 LRDIKDFMRVSLTLTLISLATV--DGSNDHODIGLDQLQLEMRERTYLTVEATIHGLD 541
 QY 447 SLF-----INGYAPONLS-IRG-----EYQIFPHVMNLSNPPTSSEYITLLRDIQD 494
 Db 542 KIMDAKPLVNGREIMQIAELKKGSRILREWQK--LITWQLAYPMTAECEKEMKRDILKA 599
 QY 495 K 495
 Db 600 K 600

RESULT 11
 ENGI YEAST STANDARD; PRT; 1117 AA.
 AC P53753;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 07-MAR-2006, entry version 35.
 DE Endo-1,3(4)-beta-glucanase 1 precursor (BC 3.2.1.6) (Endo-1,4-beta-glucanase 1) (Endo-1,3-beta-glucanase 1) (Laminarinase-1).
 GN Name=DSE4; Synonym=ENGI; OrderedlocusNames=YNR067C; ORFNames=N3547;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA MEDLINE=97313269; PubMed=9169873;
 RA Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K., Hegemann J.H., Obermaier B., Urrutiarazu L.A., Aert R., Albertmann K., Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M., Belhauer J.D., Boskovic J., Builrago M.J., Buserreau F., Coster F., Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F., Daignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M., Fritz C., Galliardin C., Garcia-Cantalejo J.M., Glandsdorf N., Goffeau A., Guelener U., Herbert C.J., Heumann K., Heuss-Neitzel D., Hilbert H., Hinni K., Itagaki Housasini I., Jaquet M., Jimenez A., Joniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lapingle A., Levesque H., Lyck R., Maftah M., Mallet L., Maurer C.T.C., Messenguy F., Mewes H.-W., Moestl D., Naer F., Nicaud J.-M., Nideghal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J., Pohl T.M., Punnelle B., Rebischung C., Remacha M.A., Revelle J.L., Rime M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M., Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhaesselt P., Viendeels F., Vissers S., Voet M., Volckaert G., Wach A., Wandut R., Weidner H., Zollner A., Hani U.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV and its evolutionary implications.";
 RL Nature 387:93-98(1997).
 RN [2]
 RP FUNCTION, SUBCELLULAR LOCATION, AND GLYCOSYLATION.
 RA PubMed=12455695;
 RA Baladron V., Ufano S., Duenas E., Martin-Cuadrado A.B., del Rey F., Vazquez de Aldana C.R.;
 RT "Eng1p, an endo-1,3-beta-glucanase localized at the daughter side of the septum, is involved in cell separation in Saccharomyces cerevisiae.";
 RL Eukaryot. Cell 1:774-786(2002).

RN [3]
 RP LEVEL OF PROTEIN EXPRESSION.
 RA MEDLINE=22923965; PubMed=14562106; DOI=10.1038/nature02046;
 RA Ghemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A., Dephoure N., O'Shea E.K., Weissman J.S.;
 RT "Global analysis of protein expression in yeast.";
 RL Nature 425:737-741(2003).
 CC -1- FUNCTION: Involved in the dissolution of the mother-daughter septum during cell separation.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,3- or 1,4-linkages in beta-D-glucans when the glucose residue whose reducing group is involved in the linkage to be hydrolyzed is itself substituted at C-3.
 CC -1- SUBCELLULAR LOCATION: Cell wall. Localizes asymmetrically to the daughter side of the septum.
 CC -1- PTM: Glycosylated.
 CC -1- MISCELLANEOUS: Present with 64 molecules/cell.
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 81 family.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: Z71682; CAA96349.1; -; Genomic DNA.
 CC PIR: S63399; S63399.
 CC Germonline: 143412; -;
 CC Ensembl: YNR067C; Saccharomyces cerevisiae.
 CC GenomeReviews: Y13139_GR; YNR067C.
 CC DR SGD: S000005350; DSE4.
 CC DR LinkDb; SCER-528-01:SCER-528-01-005268-MONOMER; -;
 CC DR LinkHub; P53753; -;
 CC DR GO: GO:0030428; C:cell septum; IDA.
 CC DR GO: GO:0009277; C:cell wall (sensu Fungi); IDA.
 CC DR GO: GO:0007109; F:cytokinesis, completion of separation; IEPI.
 CC DR InterPro: IPR005200; Glyco_hydro_81.
 CC DR Pfam: PF03639; Glyco_hydro_81; 1.
 CC KW Complete proteome; Glycoprotein; Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 16 Potential
 FT CHAIN 17 1117 Endo-1,3(4)-beta-glucanase 1.
 FT FT /FTid=PRO_0000012133.
 FT COMPBIAS 342 345 Poly-Ser.
 FT COMPBIAS 365 370 Poly-Ser.
 FT COMPBIAS 376 383 Poly-Ser.
 FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 280 280 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 533 533 N-linked (GlcNAc...) (Potential)
 FT CARBOHYD 886 886 N-linked (GlcNAc...) (Potential)
 SQ SEQUENCE 1117 AA; 121064 MW; 87F13A07E42B0AD1 CRC64;

Query Match 3.4%; Score 135.5; DB 1; Length 1117;
 Best local Similarity 21.1%; Pred. No. 6.9;
 Matches 156; Conservative 94; Mismatches 255; Indels 233; Gaps 39;

QY 4 PARPARRTKLTHRSSVSTSTPGPPYVLA-----SKTPAS--IFGPAASHL 51
 Db 206 PYSYSGEIKIIP---SLTSNKTITITISVTRMAARATGDSFIASIPASTLPYPNSNTD 263
 QY 52 LILFLNFTTNLRYEEN-----MWPGRKKNTERV-----LQGLRLP 91
 Db 264 LVQ-TLASTSPAPVPSNRQITLSPVSIVSTSPISPIVSNITENGSSPSSLSTVSPV 322
 QY 92 FKNTSVGLVGCCTULLRPKDGEARTGVDAICHRPPPTGGLDRQLYELS-QTHS 150
 Db 323 YPSSSTGNIL---LSSLFTVDSST-----PVSSITD--TIYVSSSQATIS 365
 QY 151 ITTEGPLYLDSDLYVNGFTTRSSVPTTSGVSEEPFTLFTTNLRMYADMCGPGSLK 210
 Db 366 SSSSRQTKTSSS-----SLSTSTSTATTENSTT--TIVNLFNAVSTDEPPIV- 414

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

[illegible]

QY 560 QLV-----IHTEMESSVQPTSSSTQHVFNTLNLPSQDKAQPNTNQR 610
DB 833 SVFNLPKAPTKLIPYSTNGKSVYIPKSNQ--PSLNTNSNIPLSPEDKO-----WVL 884
QY 611 NKRNIEDALNQLFRNSSIKSYFSDCVSTFRSVPNRHHTGVSL-----CNFSPLARVD 665
DB 885 KLSKSGVNDRLDMKIFILADYIYHSSKS-----TSPAKADPELPDINTP--RVVF 936
QY 666 RVAIIEEPLRMTRNGTQLOQLNFTLDRSSVLVDGYSPPNRNEPLTGSNADIQHSGRSSLEG 725
DB 937 FEVCYKSEPFSSGSGTAETNF-----ESV-----HTLSNKKDESDSTRGLNSLIP 982
QY 726 REQKLI-----BEDLNMHTGHHH 747
DB 983 NFGKVKVSLQTVQANVFGEIDTSHDSSFNASSSHHHH 1020
RESULT 13
ID Q54E23_DICDI PRELIMINARY; PRT; 797 AA.
AC Q54E23;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE 21-FEB-2006, entry version 7.
GN Hypothetical protein AAC1.
OS Name=AAC1; ORFNames=DD80201568;
OC Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Suggang R., Barriman M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Tunngang R., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Banier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren B., Davis P.,
RA Kerthouren A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrocher P., Desany B., Just E., Morio T., Roat R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wainwright A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louised H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shalaby G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
CC EMBL, AAF1000264; EAL61460.1; -; genomic_DNA.
DB InterPro; IPR001611; LRR.
DB InterPro; IPR007091; LRR_RNinh.
DB InterPro; IPR003590; LRR_RNinh_sub.
DB Pfam; PF00560; LRR_1; 2.
DB PRINTS; PR00019; LRR_RNinh.
DB Hypothetical protein; Leucine-rich repeat; Repeat.
KW SEQUENCE 797 AA; 89497 MW; 0CCB0676C5C581FF CRC64;
Query Match 3.4%; Score 132.5; DB 2; Length 797;
Best Local Similarity 19.2%; Pred. No. 6; 6;
Matches 173; Conservative 118; Mismatches 311; Indels 299; Gaps 42;

QY 6 RARRTKLTFRSSVSTSTPGPTVYLGAASKTPASIPGSAASHLLILFTLNTITNLR 65
DB 3 RTSNRNEATAKLSSSTITTTTNNKYNNMAAES-----SKSTTISNLI 48
QY 66 YEENMPGSRKFNTERVLOGLRPLFRNTSVGLPYSGCRLLLRPEKDEA-----TGV 120
DB 49 PKYSLFENPNNDNT-----NSSTRP-----NKQOKLKSNESTSTTTTTP 92
QY 121 DAICHRDPFGPGDGR---EQYLIELSQLTHSTELGAPYLLDSDSLVNGFTTHSSVPT 177
DB 93 TTTTNTTTTTPMLSKYNNVLYIEKONEKONL-----PTTETTTTTPTLTTT 148
QY 178 TSTGVSE-----PTL-----NFTINN 196
DB 149 TTTTNTTQIQTSTTSTINHLPLIQKEITFLVELGSLNARKVCKWKKVNGCVEN 208
QY 197 LR-YWADMGQPSLKFNTIDNMKHLSPFLQSSLGARYTCRVIALRSYKNGAETRV 255
DB 209 LNIYFTDHLASVX-HVSEVFKSLNSDYFHLQSV-----SFLNGAKNSIS 254
QY 256 LLCTYLOPLSGP-----GLPIKQVHELSQTHGIGTRIGPSLSDKS 297
DB 255 YSEEFNNVILPFIENVRYNQTLENFTIKGFPITRINKSSQOL-----LPYVLYHST 309
QY 298 LYINGVNERGPDDEPTPKP-----ATPLPLSEATTAGYHLKT----- 338
DB 310 SVSPSPPPPPPPPPQIQOPTTPTAPTSTTAAVSTTTTAAAGQTLNNNNNNNNIPKGLNY 369
QY 339 -LTINFTISNLYSPDMKGSAT-----FNSTEGVLOHLRLPLFKSMGPPYLGQSLIS 392
DB 370 YLTNNFKLKIKNLKR-NIGLDSRDKPDFSSLSGVSNNLTETLIICDNIQD--EGQQLLSV 426
QY 393 -----LPEKDGAAATGVDTTCTHPDPVGPGLDIQOLYWEISQLTHGVTLQGF 440
DB 427 ILIKMLKVLRLLELOKN-----OPTNSAYVILNKV--LSCBQLQLETLNLSN----- 473
QY 441 YVLDSDSLFI--NGVAPQNLISIRGEYQINFIHVMNLSNPPTSEVITLLRDIDKVT 498
DB 474 -RIDEQGLIMKDGFG-RNKSLE-----EFLPSKRLGNTDSV-----DFGKSITS 517
QY 499 LYKGSQSLHDT-----FRFCIVTNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTL 548
DB 518 L-----DLHDSVNGSKSISIKGLSOLYIKFVESTISLNTLSNHIHGSNALSLSKSPVNTQL 573
QY 549 ---NASFWLGSYQL-----VDIHTEMESSVYQPTS-----SSSTQHF-- 585
DB 574 KFDVLSFVKINSNFDLHVLSSLIINSHISISIQSNQIDWNTSAITLSQLFNSRQLFSP 633
QY 586 --YLN-----FTITNLPSQDKAQPNTNQRKRNIEDALNQLF 623
DB 634 FKYINLSGNKIGIGLKKLINDLSKYSKTHIYNNNDNNNNKKNENKSKIK--NLSE 690
QY 624 RNSS-----IKSYFSDCVSTFRSVPNRHHTGVDSLGNFSPLARVDVAIYEEFLMT 677
DB 691 NNNNNNFYKIKIKNYHD--TPIIKTINNSGNKL-----LBEVGVQ-----INSS 734
QY 678 NNGTQLONFLDRSSVLVDGYSPPNRNEPLTGSNADIQHSGRSSLEG-----PRFQK 730
DB 735 SNDTN-QQNDN-----NNENNLTETISLD-----SSNSPLEVSKVIGLIPRYSK 778
QY 731 L 731
DB 779 L 779
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Q2PZL6_MOUSE PRELIMINARY; PRT; 4981 AA.
ID Q2PZL6_MOUSE
AC Q2PZL6;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DB Fat4.

GN Name=Fat4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NCBIROTIDE SEQUENCE.
 RA Qi C., Zhu Y.T., Hu L., Zhang Z., Rao S.M., Zhu Y.-J.;
 RT "Identification of Fat4 as the candidate tumor suppressor gene in
 RT breast cancers through random chromosome deletion."
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (By similarity).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: DQ286572; AB888946.1; -; mRNA.
 DR Calcium; Cell adhesion; EGF-like domain; Membrane; Repeat;
 KW Transmembrane.
 SQ SEQUENCE 4981 AA; 540343 MW; 5AC7C40F5C5A500 CRC64;
 Query Match 3.4%; Score 132.5; DB 2; Length 4981;
 Best Local Similarity 20.1%; Pred. No. 1e+02;
 Matches 165; Conservative 107; Mismatches 299; Indels 249; Gaps 40;
 Oy 40 ASIRPSSAASHLLILFTINFTINLRVEMNPPGSRKNTTER-VLOGLRPLPKNTSV 97
 Db 1587 ASALVPSQ-----LTVNLIVATDIDGPR-----RRKSTTELYVILQGLGDPVFTQKY 1634
 Oy 98 GLVSGCGLTLRLPEKDEATGVDAICTHRDPPTGPG----- 134
 Db 1635 -----ITLL--KEGEPIGTNVISIEASPGSGEPVEYIVSVRCERTVGRIFTI 1683
 Oy 135 -----LDREQ--LYLEISQTHSITELGPYTLDRDLSLYNGFTHRSSVPTTS 179
 Db 1684 GRTGVIGTAAILDRGQACLYL-----VDVVAIKSSAPR--TORAVEITL 1730
 Oy 180 TGVVSEEPF-----TLNFTINLRVAMDMGQSLKFNITDVMNKLSPLRQSSLGARY 235
 Db 1731 QDINDNPVPFPTDILDLVEE-----NIGDG-----SKINQLTAMDMD- 1768
 Oy 236 TGCRIYALRSVNGAET--RYDLCTYLOPLSGPGLPKQYFHELSQOHTGTRLGPSYL 293
 Db 1769 EGAAALVYALISGADBSFRID-----PESGDIATKRDRERKRYSLVRAAD-GL 1820
 Oy 294 DKDSLILYNGNEPGDEPPTTPKPAATFLPPLSEATTAMGYHLKTLT-----INFTISN 347
 Db 1821 QSDMRINITISDVNDHTRPSRPSVYSF--DIPEDTTGSLVAAILATDDDSGVNGEISY 1878
 Oy 348 LQYSPDMKGSATFTSTGCVLOHLRLPFOKSSMGPFILGCOLISLRKKGAAATGVTT 407
 Db 1879 V-VEERDDGQVFLNLVTGVF-NLTRALDYETQQ--YV-----ILTVRAEDGG--GOSTT 1927
 Oy 408 -----CTYHPD-----PYGPGLDIQOLYWEISQTHGV-TOLGPGYV 442
 Db 1928 IRAYNIIDVANDNPVFSMSISYSLMNLDPGISTV---LVFNTVTDADGVNGLSISYI 1983
 Oy 443 LDRDSLFTNGYAPQWLSIRGEYOINFHIVNMNLSNPDTSSRYITLLRIDP-----K 495
 Db 1984 ASGDSL-----GQPAVDKGVLKTKLKALDRBSQGFYVLVIOVHDLPPGPTSR 2030
 Oy 496 VTTLYKGS---QLHDTFRFLCYVTLT-----MDSLVLYVKALPSSNLDPSLVGEVFL 544
 Db 2031 FTSTAQVSIILLDVANDNPMPFLSPKLTLYI PRNTPTIDTVFPAKQADPDGSPSYIEYTL 2090
 Oy 545 DK-----TLNAGFHWLG-----STYOLVDIHVEMSSVYOPTSSSTQ--HFYL 587
 Db 2091 NPSGKKSIGITIDGVALTGELDRREVSNTSL-----TVVATDKQKQPPSLSTEVVAVL 2145
 Oy 588 NFTITLPSYQ-----DKAQPTTYQNRKNIEIDALNQLFENSSIKSYFSDQVST 639

Db 2146 DINDNNEVFAQMYRVOIKENILITGDIQVSAADNDEGTNGOVRIGVG----- 2196
 Oy 640 FRSPVNRHHT-GVDSLCSFSPILARRVR--VAIYEELMTNRTGTOQLNFTLDRSSVLVD 696
 Db 2197 -----NTHQFRIDSVYGAITVAKSLDRERTPTVTLVQATIDRSGSPRTSGTVAITLLD 2251
 Oy 697 -----GSPNNEPPLTNGNSADIQHSGGRSLIEGP 725
 Db 2252 MNDFVPVPELSPYSVNPENILGTLPRAILQVARDDDQGP 2291
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 ID 054B54 D1CDI PRELIMINARY; PRT; 1230 AA.
 AC 054B54;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Hypothetical protein.
 DE ORENames=DD80184069;
 GN Dictyostelium discoideum (Slime mold).
 OS Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 OC NCBI_TaxID=44689;
 RN [1]
 RP NCBIROTIDE SEQUENCE.
 RP STRAIN=AX4;
 RX PubMed=15875012; DOI=10.1038/nature03481;
 RA Eichinger L., Pechebat J.A., Gloeckner G., Rajandream M.A., Xu O.,
 RA Sugang R., Berriman M., Song J., Olsen R., Safranek K., Xu O.,
 RA Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
 RA Cooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,
 RA Muny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Salto T.,
 RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
 RA Knights A., Loulès H., Mungall K.L., Oliver K., Price C.,
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitch B., Steffen D.,
 RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
 RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
 RA Tanaka Y., Shaulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
 RA Cox B.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
 RA Kupe A.;
 RT "The genome of the social amoeba Dictyostelium discoideum."
 RL Nature 435:43-57(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: AAF01000263; EAL61520.1; -; Genomic_DNA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00023; Ank; 3.
 DR Pfam: PF00904; Involucrin; 2.
 DR PRINTS: PRO1415; ANKYRIN.
 DR SMART: SMO0248; ANK; 2.
 DR PROSITE: PS50297; ANK_REPEAT; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 1.
 KW ANK repeat; Hypothetical protein; Repeat.
 SQ SEQUENCE 1230 AA; 139239 MW; 6F9B094941E6BD2C CRC64;
 Query Match 3.3%; Score 131; DB 2; Length 1230;
 Best Local Similarity 18.5%; Pred. No. 16;
 Matches 127; Conservative 96; Mismatches 244; Indels 218; Gaps 29;
 Oy 137 REQYLELSQTHSITELGPYTLDRDLSLYNGFTHRSSVPTTSGVSE-----PTLN 191

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 14, 2006, 04:04:35 ; Search time 54 Seconds
(without alignments)
1212.461 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAGPARARTRKLFTHRSSV.....QKLISEDLNMTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/1aa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/1aa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/1aa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/1aa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/1aa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3663	92.9	833	2 US-09-404-879A-389	Sequence 389, App
2	3663	92.9	833	2 US-09-667-857-389	Sequence 389, App
3	3663	92.9	833	2 US-10-198-053-389	Sequence 389, App
4	3663	92.9	833	2 US-09-827-271-389	Sequence 389, App
5	3663	92.9	914	2 US-09-404-879A-312	Sequence 312, App
6	3663	92.9	914	2 US-09-338-933-312	Sequence 312, App
7	3663	92.9	914	2 US-09-667-857-312	Sequence 312, App
8	3663	92.9	914	2 US-10-198-053-312	Sequence 312, App
9	3663	92.9	914	2 US-10-198-053-312	Sequence 478, App
10	3663	92.9	914	2 US-09-827-271-312	Sequence 312, App
11	3651	92.5	3451	2 US-10-198-053-595	Sequence 595, App
12	3642	92.3	1148	2 US-10-198-053-458	Sequence 458, App
13	3642	92.3	1148	2 US-10-198-053-458	Sequence 479, App
14	3642	92.3	1148	2 US-09-827-271-458	Sequence 458, App
15	3642	92.3	1156	2 US-10-198-053-459	Sequence 459, App
16	3642	92.3	1156	2 US-09-827-271-459	Sequence 459, App
17	3189	80.8	772	2 US-09-404-879A-388	Sequence 388, App
18	3189	80.8	772	2 US-09-667-857-388	Sequence 388, App
19	3189	80.8	772	2 US-10-198-053-388	Sequence 388, App
20	3189	80.8	772	2 US-09-827-271-388	Sequence 388, App
21	1996	50.6	438	2 US-10-198-053-483	Sequence 483, App
22	1990	50.4	438	2 US-09-667-857-390	Sequence 390, App
23	1990	50.4	438	2 US-10-198-053-390	Sequence 390, App
24	1990	50.4	438	2 US-09-827-271-390	Sequence 390, App
25	1990	50.4	438	2 US-10-198-053-486	Sequence 486, App
26	1436	36.4	304	2 US-10-198-053-486	Sequence 486, App

27	1345	34.1	318	2 US-10-198-053-594	Sequence 594, App
28	903	22.9	178	2 US-10-198-053-489	Sequence 489, App
29	903	22.9	233	2 US-10-198-053-488	Sequence 488, App
30	842.5	21.4	294	2 US-10-198-053-487	Sequence 487, App
31	814	20.6	313	2 US-10-198-053-461	Sequence 461, App
32	814	20.6	313	2 US-09-827-271-461	Sequence 461, App
33	809	20.5	155	2 US-10-198-053-591	Sequence 591, App
34	800	20.3	150	2 US-10-198-053-593	Sequence 593, App
35	697	17.7	134	2 US-10-198-053-592	Sequence 592, App
36	675.5	17.1	210	2 US-10-198-053-481	Sequence 481, App
37	662	16.8	230	2 US-10-198-053-480	Sequence 480, App
38	659.5	16.7	156	2 US-10-198-053-589	Sequence 589, App
39	651.5	16.5	156	2 US-10-198-053-596	Sequence 596, App
40	637.5	16.2	156	2 US-10-198-053-590	Sequence 590, App
41	611.5	15.5	288	2 US-10-198-053-485	Sequence 485, App
42	607.5	15.4	156	2 US-10-198-053-584	Sequence 584, App
43	600.5	15.2	156	2 US-10-198-053-587	Sequence 587, App
44	599.5	15.2	156	2 US-10-198-053-583	Sequence 583, App
45	598.5	15.2	156	2 US-10-198-053-586	Sequence 586, App

ALIGNMENTS

RESULT 1

US-09-404-879A-389
Sequence 389, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 389
LENGTH: 833
TYPE: PRT
ORGANISM: Homo sapiens
US-09-404-879A-389

Query Match 92.9%; Score 3663; DB 2; Length 833;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTTPGPTTVYLGAASKTPASIFGPAASHLLILFTLNTTNLRYEENWPG 73
DB	78	FTHRSSVSTTTPGPTTVYLGAASKTPASIFGPAASHLLILFTLNTTNLRYEENWPG 137
QY	74	SRKENTTEVLQGLRPLFKNTSVGLYSGCRTLRLPRKDGATVDALCTHRPPTGP 133
DB	138	SRKENTTEVLQGLRPLFKNTSVGLYSGCRTLRLPRKDGATVDALCTHRPPTGP 197
QY	134	GLDREOLYELSQLTSHITELGPTTLDRDSLVLVNGFTHRSSVPTTSTGVSEEPFTLNFT 193
DB	198	GLDREOLYELSQLTSHITELGPTTLDRDSLVLVNGFTHRSSVPTTSTGVSEEPFTLNFT 257
QY	194	INNLRYMADMGPGSLIKENITDNVMKHLISPLFORSSIGARYTGCRVIALRSVNGAETR 253
DB	258	INNLRYMADMGPGSLIKENITDNVMKHLISPLFORSSIGARYTGCRVIALRSVNGAETR 317
QY	254	VLLLCYVLPPLSGPGPIKOVFHELSQOHTGTRIGPVSLLDQSLVLNGBGDPDEPT 313
DB	318	VLLLCYVLPPLSGPGPIKOVFHELSQOHTGTRIGPVSLLDQSLVLNGBGDPDEPT 377
QY	314	TRKPAATFPPLSEATTANGYHLKTLTLNFTTSLNLOYSFDMGKSGATFNSTEGVLQHLRL 373
DB	378	TRKPAATFPPLSEATTANGYHLKTLTLNFTTSLNLOYSFDMGKSGATFNSTEGVLQHLRL 437

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QY 374 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTHPPDVPGLDIQOLYWEISQULH 433
DB 438 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTHPPDVPGLDIQOLYWEISQULH 497
QY 434 GVTQGLFYVLDKDSLFINGYAPQNLSIRGEYQINFIHVMNLSNDPPTSSSEYITLLRDIO 493
DB 498 GVTQGLFYVLDKDSLFINGYAPQNLSIRGEYQINFIHVMNLSNDPPTSSSEYITLLRDIO 557
QY 494 DKVTLLYKGSQULHDFRCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKETLNASH 553
DB 558 DKVTLLYKGSQULHDFRCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKETLNASH 617
QY 554 WIGSTYQVLDIVHTMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNQRNR 613
DB 618 WIGSTYQVLDIVHTMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNQRNR 677
QY 614 NIEDALNOLFRRNSIKSYFSDCVSTFRSVPNRHHTGVDSLGNFSLARVDVAIYEEF 673
DB 678 NIEDALNOLFRRNSIKSYFSDCVSTFRSVPNRHHTGVDSLGNFSLARVDVAIYEEF 737
QY 674 LAMTRNGTQLONFITLDRSSVLVDGYSPPNRNEPLTGN 710
DB 738 LAMTRNGTQLONFITLDRSSVLVDGYSPPNRNEPLTGN 774

RESULT 2
US-09-667-857-389
/ Sequence 389, Application US/09667857
/ Patent No. 669664
/ GENERAL INFORMATION:
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: King, Gordon E.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Fling, Steven P.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary Richard
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darick
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C5
/ CURRENT APPLICATION NUMBER: US/09/667,857
/ CURRENT FILING DATE: 2000-09-20
/ NUMBER OF SEQ ID NOS: 455
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 389
/ LENGTH: 833
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-667-857-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPTGPTVYLGASKTTPASIFGSAASHLLILFTLNTITNLRYEENMWP 73
DB 78 FTHRSSVSTSTPTGPTVYLGASKTTPASIFGSAASHLLILFTLNTITNLRYEENMWP 137
QY 74 SRKFNTERVLOGLRLPFRNTSVGLYSGCRLLTLARPEKDGATGVDAICTHRPDTGP 133
DB 138 SRKFNTERVLOGLRLPFRNTSVGLYSGCRLLTLARPEKDGATGVDAICTHRPDTGP 197
QY 134 GLDRBOLYLELSQULHSITELGPTLDRDSLTVNGFTHRSSVPTTSGVSEBPTLNT 193
DB 198 GLDRBOLYLELSQULHSITELGPTLDRDSLTVNGFTHRSSVPTTSGVSEBPTLNT 257
QY 194 INNLRYADMGQGSLSKFNTITDNVMKHLSPLFORSLSGARVYTCRVIARLRYNGAETR 253
DB 258 INNLRYADMGQGSLSKFNTITDNVMKHLSPLFORSLSGARVYTCRVIARLRYNGAETR 317
QY 254 VDLCTLYQLPSGGLPIKQVFHELSQOTGHTLGLGYSLDKDSLTVNGVNEPDPDEPT 313

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DB 318 VDLCTLYQLPSGGLPIKQVFHELSQOTGHTLGLGYSLDKDSLTVNGVNEPDPDEPT 377
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DB 378 TPKPATTEPLPLSEATTMGMHLKTLTLNFTISNLQVSPDMKGSAATNTEGVQHLR 437
QY 374 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTHPPDVPGLDIQOLYWEISQULH 433
DB 438 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTHPPDVPGLDIQOLYWEISQULH 497
QY 434 GVTQGLFYVLDKDSLFINGYAPQNLSIRGEYQINFIHVMNLSNDPPTSSSEYITLLRDIO 493
DB 498 GVTQGLFYVLDKDSLFINGYAPQNLSIRGEYQINFIHVMNLSNDPPTSSSEYITLLRDIO 557
QY 494 DKVTLLYKGSQULHDFRCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKETLNASH 553
DB 558 DKVTLLYKGSQULHDFRCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKETLNASH 617
QY 554 WIGSTYQVLDIVHTMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNQRNR 613
DB 618 WIGSTYQVLDIVHTMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNQRNR 677
QY 614 NIEDALNOLFRRNSIKSYFSDCVSTFRSVPNRHHTGVDSLGNFSLARVDVAIYEEF 673
DB 678 NIEDALNOLFRRNSIKSYFSDCVSTFRSVPNRHHTGVDSLGNFSLARVDVAIYEEF 737
QY 674 LAMTRNGTQLONFITLDRSSVLVDGYSPPNRNEPLTGN 710
DB 738 LAMTRNGTQLONFITLDRSSVLVDGYSPPNRNEPLTGN 774

RESULT 3
US-10-198-053-389
/ Sequence 389, Application US/10198053
/ Patent No. 6858710
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C9
/ CURRENT APPLICATION NUMBER: US/10/198,053
/ CURRENT FILING DATE: 2002-07-17
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 389
/ LENGTH: 833
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-198-053-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 78 FTHRSSVSTSTPTGPTVYLGASKTTPASIFGSAASHLLILFTLNTITNLRYEENMWP 137
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DB 138 SRKFNTERVLOGLRLPFRNTSVGLYSGCRLLTLARPEKDGATGVDAICTHRPDTGP 197
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DB 198 GLDRBOLYLELSQULHSITELGPTLDRDSLTVNGFTHRSSVPTTSGVSEBPTLNT 257
QY 194 INNLRYADMGQGSLSKFNTITDNVMKHLSPLFORSLSGARVYTCRVIARLRYNGAETR 253
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QY 314 TPKPATTFLPPLSEATTAMGYHLKTLINFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
DB 378 TPKPATTFLPPLSEATTAMGYHLKTLINFTISNLQYSPDMGKSATFNSTEGVLOHLR 437
QY 374 PLFOKSMGPFYIGCOLISIRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYBELSOLTH 433
DB 438 PLFOKSMGPFYIGCOLISIRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYBELSOLTH 497
QY 434 GTVQLGFYVLDRLSLFNGAPONLSIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIO 493
DB 498 GTVQLGFYVLDRLSLFNGAPONLSIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIO 557
QY 494 DKYTTLYKGSQDLHDTFRFCVLTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 558 DKYTTLYKGSQDLHDTFRFCVLTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASFH 617
QY 554 WLGSTYQVLDIHVTEMESSYVQPTSSSTQHFIYLNFTITNLPSQDKAOGTTNYQRNKR 613
DB 618 WLGSTYQVLDIHVTEMESSYVQPTSSSTQHFIYLNFTITNLPSQDKAOGTTNYQRNKR 677
QY 614 NIEDANOLFNRNSIKSYSDCOVSTFRSVPNRHHTGVDSL CNFSLARRVDVAIYEER 673
DB 678 NIEDANOLFNRNSIKSYSDCOVSTFRSVPNRHHTGVDSL CNFSLARRVDVAIYEER 737
QY 674 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 710
DB 738 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 774

RESULT 4

US-09-827-271-389
; Sequence 389, Application US/09827271
; Patent No. 6662980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENMMPG 73
DB 78 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENMMPG 137
QY 74 SRKFNTTERVLQGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 138 SRKFNTTERVLQGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 197
QY 134 GLDREQLYELSQLTHSITELEGPYTLDRDSL YVNGFTHRSSVPTSTGVVSEBPFLLNFT 133
DB 198 GLDREQLYELSQLTHSITELEGPYTLDRDSL YVNGFTHRSSVPTSTGVVSEBPFLLNFT 257
QY 194 INNLRYADMGQGSGLKFNITDVMKHLISPLFORSSLGARYTGCRVIALRSYKNGAETR 253
DB 258 INNLRYADMGQGSGLKFNITDVMKHLISPLFORSSLGARYTGCRVIALRSYKNGAETR 317

QY 254 VDLICTYLOPLSGRGLPIKOVFHELISOOTHGIRLGPYSLDKOSLYLNGYNEBPGDPPT 313
DB 318 VDLICTYLOPLSGRGLPIKOVFHELISOOTHGIRLGPYSLDKOSLYLNGYNEBPGDPPT 377
QY 314 TPKPATTFLPPLSEATTAMGYHLKTLINFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
DB 378 TPKPATTFLPPLSEATTAMGYHLKTLINFTISNLQYSPDMGKSATFNSTEGVLOHLR 437
QY 374 PLFOKSMGPFYIGCOLISIRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYBELSOLTH 433
DB 438 PLFOKSMGPFYIGCOLISIRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYBELSOLTH 497
QY 434 GTVQLGFYVLDRLSLFNGAPONLSIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIO 493
DB 498 GTVQLGFYVLDRLSLFNGAPONLSIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIO 557
QY 494 DKYTTLYKGSQDLHDTFRFCVLTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 558 DKYTTLYKGSQDLHDTFRFCVLTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASFH 617
QY 554 WLGSTYQVLDIHVTEMESSYVQPTSSSTQHFIYLNFTITNLPSQDKAOGTTNYQRNKR 613
DB 618 WLGSTYQVLDIHVTEMESSYVQPTSSSTQHFIYLNFTITNLPSQDKAOGTTNYQRNKR 677
QY 614 NIEDANOLFNRNSIKSYSDCOVSTFRSVPNRHHTGVDSL CNFSLARRVDVAIYEER 673
DB 678 NIEDANOLFNRNSIKSYSDCOVSTFRSVPNRHHTGVDSL CNFSLARRVDVAIYEER 737
QY 674 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 710
DB 738 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 774

RESULT 5

US-09-404-879A-312
; Sequence 312, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-404-879A-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENMMPG 73
DB 159 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENMMPG 218
QY 74 SRKFNTTERVLQGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 219 SRKFNTTERVLQGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 278
QY 134 GLDREQLYELSQLTHSITELEGPYTLDRDSL YVNGFTHRSSVPTSTGVVSEBPFLLNFT 193
DB 279 GLDREQLYELSQLTHSITELEGPYTLDRDSL YVNGFTHRSSVPTSTGVVSEBPFLLNFT 338
QY 194 INNLRYADMGQGSGLKFNITDVMKHLISPLFORSSLGARYTGCRVIALRSYKNGAETR 253
DB 258 INNLRYADMGQGSGLKFNITDVMKHLISPLFORSSLGARYTGCRVIALRSYKNGAETR 317

Db 339 INNLRYMADMGQPGSLKFNITDNVWKHLISPLFORSSIGARTGCRVIALASVKNGAETR 398
 Qy 254 VDLICTYIQLPSGGLPIKOVFHELSQOHTGITRLGPVSLDKDSLVLNGYNEPGDEBPT 313
 Db 399 VDLICTYIQLPSGGLPIKOVFHELSQOHTGITRLGPVSLDKDSLVLNGYNEPGDEBPT 458
 Qy 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQVSPDMKGASATFNSTEGVLOHLIR 373
 Db 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQVSPDMKGASATFNSTEGVLOHLIR 518
 Qy 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTTHAPDPVGPGLDLOQLYWEISQOLTH 433
 Db 519 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTTHAPDPVGPGLDLOQLYWEISQOLTH 578
 Qy 434 GVTOLGFVYLRDLSLFINGYAPONLSIRGEYOINPHIYVNMNLSNPDPTSSSEYITLLRDIO 493
 Db 579 GVTOLGFVYLRDLSLFINGYAPONLSIRGEYOINPHIYVNMNLSNPDPTSSSEYITLLRDIO 638
 Qy 494 DKVTLTYKGSQULHDFRCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASHF 553
 Db 639 DKVTLTYKGSQULHDFRCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASHF 698
 Qy 554 WLGSTYQULVDIHVTEMESSVYQPTSSSTOHPFLNFTITNLPSODKAPGTTNYQRNKR 613
 Db 699 WLGSTYQULVDIHVTEMESSVYQPTSSSTOHPFLNFTITNLPSODKAPGTTNYQRNKR 758
 Qy 614 NIEDALNOLFNRSSIKSYFSDCOVSTFRSVPRNRHHTGVDSLGNFSLARRVDVAIYEEF 673
 Db 759 NIEDALNOLFNRSSIKSYFSDCOVSTFRSVPRNRHHTGVDSLGNFSLARRVDVAIYEEF 818
 Qy 674 LRMTNRGTOLQNFLLDRSSVLVDGYSFNRNEPLTGN 710
 Db 819 LRMTNRGTOLQNFLLDRSSVLVDGYSFNRNEPLTGN 855

RESULT 6
 US-09-338-933-312
 / Sequence 312, Application US/09338933
 / Patent No. 6488931
 / GENERAL INFORMATION:
 / APPLICANT: Mitcham, Jennifer Lynn
 / APPLICANT: King, Gordon B.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
 / TITLE OF INVENTION: OVARIAN CANCER
 / FILE REFERENCE: 210121.462C1
 / CURRENT APPLICATION NUMBER: US/09/338,933
 / CURRENT FILING DATE: 1999-06-23
 / NUMBER OF SEQ ID NOS: 312
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 312
 / LENGTH: 914
 / TYPE: PR1
 / ORGANISM: Homo sapien
 / US-09-338-933-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGPTPVYVIGASTPASIIPSPASASHLLILFTLNFTITNLRYEENMPG 73
 Db 159 FTHRSSVSTSTGPTPVYVIGASTPASIIPSPASASHLLILFTLNFTITNLRYEENMPG 218
 Qy 74 SRKNTTERTVLOGLRLPLFKNTSVGPLYSGCRLTLRLPEKXGEATGVDAICTHRPDPGP 133
 Db 219 SRKNTTERTVLOGLRLPLFKNTSVGPLYSGCRLTLRLPEKXGEATGVDAICTHRPDPGP 278
 Qy 134 GLDREOLYELSQLTHSTTELGPTLDRDSLVLNGFTHRSVPTTSGVSEBPTLNFT 193
 Db 279 GLDREOLYELSQLTHSTTELGPTLDRDSLVLNGFTHRSVPTTSGVSEBPTLNFT 338
 Qy 194 INNLRYMADMGQPGSLKFNITDNVWKHLISPLFORSSIGARTGCRVIALASVKNGAETR 253

Db 339 INNLRYMADMGQPGSLKFNITDNVWKHLISPLFORSSIGARTGCRVIALASVKNGAETR 398
 Qy 254 VDLICTYIQLPSGGLPIKOVFHELSQOHTGITRLGPVSLDKDSLVLNGYNEPGDEBPT 313
 Db 399 VDLICTYIQLPSGGLPIKOVFHELSQOHTGITRLGPVSLDKDSLVLNGYNEPGDEBPT 458
 Qy 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQVSPDMKGASATFNSTEGVLOHLIR 373
 Db 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQVSPDMKGASATFNSTEGVLOHLIR 518
 Qy 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTTHAPDPVGPGLDLOQLYWEISQOLTH 433
 Db 519 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTTHAPDPVGPGLDLOQLYWEISQOLTH 578
 Qy 434 GVTOLGFVYLRDLSLFINGYAPONLSIRGEYOINPHIYVNMNLSNPDPTSSSEYITLLRDIO 493
 Db 579 GVTOLGFVYLRDLSLFINGYAPONLSIRGEYOINPHIYVNMNLSNPDPTSSSEYITLLRDIO 638
 Qy 494 DKVTLTYKGSQULHDFRCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASHF 553
 Db 639 DKVTLTYKGSQULHDFRCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASHF 698
 Qy 554 WLGSTYQULVDIHVTEMESSVYQPTSSSTOHPFLNFTITNLPSODKAPGTTNYQRNKR 613
 Db 699 WLGSTYQULVDIHVTEMESSVYQPTSSSTOHPFLNFTITNLPSODKAPGTTNYQRNKR 758
 Qy 614 NIEDALNOLFNRSSIKSYFSDCOVSTFRSVPRNRHHTGVDSLGNFSLARRVDVAIYEEF 673
 Db 759 NIEDALNOLFNRSSIKSYFSDCOVSTFRSVPRNRHHTGVDSLGNFSLARRVDVAIYEEF 818
 Qy 674 LRMTNRGTOLQNFLLDRSSVLVDGYSFNRNEPLTGN 710
 Db 819 LRMTNRGTOLQNFLLDRSSVLVDGYSFNRNEPLTGN 855

RESULT 7
 US-09-667-857-312
 / Sequence 312, Application US/09667857
 / Patent No. 669664
 / GENERAL INFORMATION:
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: King, Gordon B.
 / APPLICANT: Algate, Paul A.
 / APPLICANT: Pling, Steven P.
 / APPLICANT: Reiter, Marc W.
 / APPLICANT: Fanger, Gary Richard
 / APPLICANT: Reed, Steven G.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
 / FILE REFERENCE: 210121.462C5
 / CURRENT APPLICATION NUMBER: US/09/667,857
 / CURRENT FILING DATE: 2000-09-20
 / NUMBER OF SEQ ID NOS: 455
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 312
 / LENGTH: 914
 / TYPE: PR1
 / ORGANISM: Homo sapien
 / US-09-667-857-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGPTPVYVIGASTPASIIPSPASASHLLILFTLNFTITNLRYEENMPG 73
 Db 159 FTHRSSVSTSTGPTPVYVIGASTPASIIPSPASASHLLILFTLNFTITNLRYEENMPG 218
 Qy 74 SRKNTTERTVLOGLRLPLFKNTSVGPLYSGCRLTLRLPEKXGEATGVDAICTHRPDPGP 133
 Db 219 SRKNTTERTVLOGLRLPLFKNTSVGPLYSGCRLTLRLPEKXGEATGVDAICTHRPDPGP 278

QY 134 GLDREQLYELSQLTHSITELGPTLDRDLSYNGFTHRSSVPTTSTGVSEEPFTLNFT 193
|||
DB 279 GLDREQLYELSQLTHSITELGPTLDRDLSYNGFTHRSSVPTTSTGVSEEPFTLNFT 338
|||
QY 194 INNLRYADMGQPSLSKFNTIDNMKHLSPFORSSIGARYTCRYALRSVNGAETR 253
|||
DB 339 INNLRYADMGQPSLSKFNTIDNMKHLSPFORSSIGARYTCRYALRSVNGAETR 398
|||
QY 254 VDLICTYLOPLSGGPIKQVFEHLSQOQTHGIRLGPYSLDKDSLXYNGNEBGPDEPPT 313
|||
DB 399 VDLICTYLOPLSGGPIKQVFEHLSQOQTHGIRLGPYSLDKDSLXYNGNEBGPDEPPT 458
|||
QY 314 TPKPATTFLPLSBATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
|||
DB 459 TPKPATTFLPLSBATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 518
|||
QY 374 PLFOKSMGPFYLGCOLISLPEKDAATGVDTTCTYHPDPVPGDLIOQLYWELSQULTH 433
|||
DB 519 PLFOKSMGPFYLGCOLISLPEKDAATGVDTTCTYHPDPVPGDLIOQLYWELSQULTH 578
|||
QY 434 GVTOLGFYVLDRLSLFINGYAPQNLIRGEYQINPHIYNNMNLSPDPTSSSEYITLLRDIQ 493
|||
DB 579 GVTOLGFYVLDRLSLFINGYAPQNLIRGEYQINPHIYNNMNLSPDPTSSSEYITLLRDIQ 638
|||
QY 494 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSELVEQVFLDKTLNLSFH 553
|||
DB 639 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSELVEQVFLDKTLNLSFH 698
|||
QY 554 WLGSYQVLDIHTHEMESSYQOPTSSSTQHFYLNFTTNLPYSQDAQOCTTYOQNR 613
|||
DB 699 WLGSYQVLDIHTHEMESSYQOPTSSSTQHFYLNFTTNLPYSQDAQOCTTYOQNR 758
|||
QY 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSLGNFPLARVDVAIYEEF 673
|||
DB 759 NIEDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSLGNFPLARVDVAIYEEF 818
|||
QY 674 LRMTNGTQLONFLDRSSVLYVDGSPNRNEPPLTGN 710
|||
DB 819 LRMTNGTQLONFLDRSSVLYVDGSPNRNEPPLTGN 855
|||

RESULT 8
US-10-198-053-312
; Sequence 312, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaityanya S.
; APPLICANT: Rafter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTGPTTVYLGASKTASIFGPAASHLLILFTLNFTTNLYEENMMPG 73
|||
DB 159 FTHRSSVSTSTGPTTVYLGASKTASIFGPAASHLLILFTLNFTTNLYEENMMPG 218
|||
QY 74 SRKNTTERVUQGLRPLFKNTSVGPIYSGCRULTLRPEKDGATGVDAICTHRPDPGP 133
|||

DB 219 SRKNTTERVUQGLRPLFKNTSVGPIYSGCRULTLRPEKDGATGVDAICTHRPDPGP 278
|||
QY 134 GLDREQLYELSQLTHSITELGPTLDRDLSYNGFTHRSSVPTTSTGVSEEPFTLNFT 193
|||
DB 279 GLDREQLYELSQLTHSITELGPTLDRDLSYNGFTHRSSVPTTSTGVSEEPFTLNFT 338
|||
QY 194 INNLRYADMGQPSLSKFNTIDNMKHLSPFORSSIGARYTCRYALRSVNGAETR 253
|||
DB 339 INNLRYADMGQPSLSKFNTIDNMKHLSPFORSSIGARYTCRYALRSVNGAETR 398
|||
QY 254 VDLICTYLOPLSGGPIKQVFEHLSQOQTHGIRLGPYSLDKDSLXYNGNEBGPDEPPT 313
|||
DB 399 VDLICTYLOPLSGGPIKQVFEHLSQOQTHGIRLGPYSLDKDSLXYNGNEBGPDEPPT 458
|||
QY 314 TPKPATTFLPLSBATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
|||
DB 459 TPKPATTFLPLSBATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 518
|||
QY 374 PLFOKSMGPFYLGCOLISLPEKDAATGVDTTCTYHPDPVPGDLIOQLYWELSQULTH 433
|||
DB 519 PLFOKSMGPFYLGCOLISLPEKDAATGVDTTCTYHPDPVPGDLIOQLYWELSQULTH 578
|||
QY 434 GVTOLGFYVLDRLSLFINGYAPQNLIRGEYQINPHIYNNMNLSPDPTSSSEYITLLRDIQ 493
|||
DB 579 GVTOLGFYVLDRLSLFINGYAPQNLIRGEYQINPHIYNNMNLSPDPTSSSEYITLLRDIQ 638
|||
QY 494 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSELVEQVFLDKTLNLSFH 553
|||
DB 639 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSELVEQVFLDKTLNLSFH 698
|||
QY 554 WLGSYQVLDIHTHEMESSYQOPTSSSTQHFYLNFTTNLPYSQDAQOCTTYOQNR 613
|||
DB 699 WLGSYQVLDIHTHEMESSYQOPTSSSTQHFYLNFTTNLPYSQDAQOCTTYOQNR 758
|||
QY 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSLGNFPLARVDVAIYEEF 673
|||
DB 759 NIEDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSLGNFPLARVDVAIYEEF 818
|||
QY 674 LRMTNGTQLONFLDRSSVLYVDGSPNRNEPPLTGN 710
|||
DB 819 LRMTNGTQLONFLDRSSVLYVDGSPNRNEPPLTGN 855
|||

RESULT 9
US-10-198-053-478
; Sequence 478, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaityanya S.
; APPLICANT: Rafter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-478

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTGPTTVYLGASKTASIFGPAASHLLILFTLNFTTNLYEENMMPG 73
|||
DB 159 FTHRSSVSTSTGPTTVYLGASKTASIFGPAASHLLILFTLNFTTNLYEENMMPG 218
|||

QY 74 SRKFTTERTVLOGGLRLPFLKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDGP 133
 DB 219 SRKFTTERTVLOGGLRLPFLKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDGP 278
 QY 134 GLDRBOLYLELSQLTSHITELGPTLDRDSLVLVNGFTHRSSVPTTSTGVASEEPTLNT 193
 DB 279 GLDRBOLYLELSQLTSHITELGPTLDRDSLVLVNGFTHRSSVPTTSTGVASEEPTLNT 338
 QY 194 INNLRYMADMGQPGSLKFNITDVMKHLSPFORSSIGARTGCRVIALRSVKNCAETR 253
 DB 339 INNLRYMADMGQPGSLKFNITDVMKHLSPFORSSIGARTGCRVIALRSVKNCAETR 398
 QY 254 VDLCTCYLOPLSGPGPIKQVHFELSQQTHGTRIGPYSLDKDSLVLVNGYNEPGDEPPT 313
 DB 399 VDLCTCYLOPLSGPGPIKQVHFELSQQTHGTRIGPYSLDKDSLVLVNGYNEPGDEPPT 458
 QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKGSAATFNSTEGVLQHLR 373
 DB 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKGSAATFNSTEGVLQHLR 518
 QY 374 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIOQLYWELSQLT 433
 DB 519 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIOQLYWELSQLT 578
 QY 434 GVTOLGFYVLDRLSLFINGYAPONTLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 493
 DB 579 GVTOLGFYVLDRLSLFINGYAPONTLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 638
 QY 494 DKVTLLYKGSQQLHDFRFLCVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 553
 DB 639 DKVTLLYKGSQQLHDFRFLCVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 698
 QY 554 WLGSTYQVLDIHYTEMESVYQPTSSSTQHFYLNFTITNLPSYQKAPGTTNYQRNR 613
 DB 699 WLGSTYQVLDIHYTEMESVYQPTSSSTQHFYLNFTITNLPSYQKAPGTTNYQRNR 758
 QY 614 NIEDALNOLFRNSSISYSDCOVSTFRSVPNRHHTGVDSLGNFSLARVDVVAIYEEF 673
 DB 759 NIEDALNOLFRNSSISYSDCOVSTFRSVPNRHHTGVDSLGNFSLARVDVVAIYEEF 818
 QY 674 LRMTNRGTOLQNTFLDRSSVLVDGSPNRPNPLTGN 710
 DB 819 LRMTNRGTOLQNTFLDRSSVLVDGSPNRPNPLTGN 855

RESULT 10
 US-09-827-271-312
 / Sequence 312, Application US/09827271
 / Patent No. 6962980
 / GENERAL INFORMATION:
 / APPLICANT: Recter, Marc W.
 / APPLICANT: Recter, Gary R.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
 / FILE REFERENCE: 210121.462C6
 / CURRENT APPLICATION NUMBER: US/09/827,271
 / CURRENT FILING DATE: 2001-04-04
 / NUMBER OF SEQ ID NOS: 461
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 312
 / LENGTH: 914
 / TYPE: PRT
 / ORGANISM: Homo sapien
 US-09-827-271-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPTGPTVYLGASTPASPISFGPSAASHLLILFTLNFTITNLRYEENMPG 73
 DB 159 FTHRSSVSTSTPTGPTVYLGASTPASPISFGPSAASHLLILFTLNFTITNLRYEENMPG 218

QY 74 SRKFTTERTVLOGGLRLPFLKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDGP 133
 DB 219 SRKFTTERTVLOGGLRLPFLKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDGP 278
 QY 134 GLDRBOLYLELSQLTSHITELGPTLDRDSLVLVNGFTHRSSVPTTSTGVASEEPTLNT 193
 DB 279 GLDRBOLYLELSQLTSHITELGPTLDRDSLVLVNGFTHRSSVPTTSTGVASEEPTLNT 338
 QY 194 INNLRYMADMGQPGSLKFNITDVMKHLSPFORSSIGARTGCRVIALRSVKNCAETR 253
 DB 339 INNLRYMADMGQPGSLKFNITDVMKHLSPFORSSIGARTGCRVIALRSVKNCAETR 398
 QY 254 VDLCTCYLOPLSGPGPIKQVHFELSQQTHGTRIGPYSLDKDSLVLVNGYNEPGDEPPT 313
 DB 399 VDLCTCYLOPLSGPGPIKQVHFELSQQTHGTRIGPYSLDKDSLVLVNGYNEPGDEPPT 458
 QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKGSAATFNSTEGVLQHLR 373
 DB 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKGSAATFNSTEGVLQHLR 518
 QY 374 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIOQLYWELSQLT 433
 DB 519 PLFOKSSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIOQLYWELSQLT 578
 QY 434 GVTOLGFYVLDRLSLFINGYAPONTLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 493
 DB 579 GVTOLGFYVLDRLSLFINGYAPONTLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 638
 QY 494 DKVTLLYKGSQQLHDFRFLCVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 553
 DB 639 DKVTLLYKGSQQLHDFRFLCVNTLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASH 698
 QY 554 WLGSTYQVLDIHYTEMESVYQPTSSSTQHFYLNFTITNLPSYQKAPGTTNYQRNR 613
 DB 699 WLGSTYQVLDIHYTEMESVYQPTSSSTQHFYLNFTITNLPSYQKAPGTTNYQRNR 758
 QY 614 NIEDALNOLFRNSSISYSDCOVSTFRSVPNRHHTGVDSLGNFSLARVDVVAIYEEF 673
 DB 759 NIEDALNOLFRNSSISYSDCOVSTFRSVPNRHHTGVDSLGNFSLARVDVVAIYEEF 818
 QY 674 LRMTNRGTOLQNTFLDRSSVLVDGSPNRPNPLTGN 710
 DB 819 LRMTNRGTOLQNTFLDRSSVLVDGSPNRPNPLTGN 855

RESULT 11
 US-10-198-053-595
 / Sequence 595, Application US/10198053
 / Patent No. 6858710
 / GENERAL INFORMATION:
 / APPLICANT: Bangur, Chaitanya S.
 / APPLICANT: Recter, Marc W.
 / APPLICANT: Recter, Gary R.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 / TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 / FILE REFERENCE: 210121.462C9
 / CURRENT APPLICATION NUMBER: US/10/198,053
 / CURRENT FILING DATE: 2002-07-17
 / NUMBER OF SEQ ID NOS: 624
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 595
 / LENGTH: 3451
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: VARIANT
 / LOCATION: 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,
 / LOCATION: 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401
 / OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-198-053-595

Query Match 92.5%; Score 3651; DB 2; Length 3451;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTGPTPTVYIGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMPG 73
DB 2696 FTHRSSVSTSTGPTPTVYIGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMPG 2755

QY 74 SRKNTTERVLOGLRLPFXNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGP 133
DB 2756 SRKNTTERVLOGLRLPFXNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGP 2815

QY 134 GLDREOLYLELSOLTHSITELGPTLDRDSL YNNGFTHRSSVPTTSIGVSEEPFTLNFT 193
DB 2816 GLDREOLYLELSOLTHSITELGPTLDRDSL YNNGFTHRSSVPTTSIGVSEEPFTLNFT 2875

QY 194 INNLRYADMGQPSLKFNTIDNVMKHLSPFORSSLGARYTCRVIALRSYKGAETR 253
DB 2876 INNLRYADMGQPSLKFNTIDNVMKHLSPFORSSLGARYTCRVIALRSYKGAETR 2935

QY 254 VDLICTYLQPLSGPGLPIKQVFHLSQQTGTRIGPYSIDKDSL YNNGYNEBGPDPPT 313
DB 2936 VDLICTYLQPLSGPGLPIKQVFHLSQQTGTRIGPYSIDKDSL YNNGYNEBGPDPPT 2995

QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSSTEGVLOHLR 373
DB 2996 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSSTEGVLOHLR 3055

QY 374 PLFOKSMGPFYIGCOLISLREKDGATGDTCTHPDPVPGGLDIQOLYMLSQLTH 433
DB 3056 PLFOKSMGPFYIGCOLISLREKDGATGDTCTHPDPVPGGLDIQOLYMLSQLTH 3115

QY 434 GVTQLGFYVLDRLSLFINGAPQNL SIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 493
DB 3116 GVTQLGFYVLDRLSLFINGAPQNL SIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 3175

QY 494 DKVTLTKGSQLHDTFRFCLVTNL TMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 553
DB 3176 DKVTLTKGSQLHDTFRFCLVTNL TMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 3235

QY 554 WLGSTYOLVDIHTEMESVYOPTSSSTOHFNFTITNL PYSDKAQPGTTNYQRNKR 613
DB 3236 WLGSTYOLVDIHTEMESVYOPTSSSTOHFNFTITNL PYSDKAQPGTTNYQRNKR 3255

QY 614 NIEDALNQLFRNSSIKSYFSDQVSTRSVPNRHHTGVDSL CNFSPILARRVDRVAIYEEF 673
DB 3296 NIEDALNQLFRNSSIKSYFSDQVSTRSVPNRHHTGVDSL CNFSPILARRVDRVAIYEEF 3355

QY 674 LRMTNGTQOLNFTLDRSSVLDGYSFNRNEPPLTGN 710
DB 3356 LRMTNGTQOLNFTLDRSSVLDGYSFNRNEPPLTGN 3392

RESULT 12
US-10-198-053-458
; Sequence 458, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaityanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-198-053-458

Query Match 92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTGPTPTVYIGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMPG 73
DB 393 FTHRSSVSTSTGPTPTVYIGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMPG 452

QY 74 SRKNTTERVLOGLRLPFXNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGP 133
DB 453 SRKNTTERVLOGLRLPFXNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGP 512

QY 134 GLDREOLYLELSOLTHSITELGPTLDRDSL YNNGFTHRSSVPTTSIGVSEEPFTLNFT 193
DB 513 GLDREOLYLELSOLTHSITELGPTLDRDSL YNNGFTHRSSVPTTSIGVSEEPFTLNFT 572

QY 194 INNLRYADMGQPSLKFNTIDNVMKHLSPFORSSLGARYTCRVIALRSYKGAETR 253
DB 573 INNLRYADMGQPSLKFNTIDNVMKHLSPFORSSLGARYTCRVIALRSYKGAETR 632

QY 254 VDLICTYLQPLSGPGLPIKQVFHLSQQTGTRIGPYSIDKDSL YNNGYNEBGPDPPT 313
DB 633 VDLICTYLQPLSGPGLPIKQVFHLSQQTGTRIGPYSIDKDSL YNNGYNEBGPDPPT 692

QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSSTEGVLOHLR 373
DB 693 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSSTEGVLOHLR 752

QY 374 PLFOKSMGPFYIGCOLISLREKDGATGDTCTHPDPVPGGLDIQOLYMLSQLTH 433
DB 753 PLFOKSMGPFYIGCOLISLREKDGATGDTCTHPDPVPGGLDIQOLYMLSQLTH 812

QY 434 GVTQLGFYVLDRLSLFINGAPQNL SIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 493
DB 813 GVTQLGFYVLDRLSLFINGAPQNL SIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 872

QY 494 DKVTLTKGSQLHDTFRFCLVTNL TMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 553
DB 873 DKVTLTKGSQLHDTFRFCLVTNL TMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 932

QY 554 WLGSTYOLVDIHTEMESVYOPTSSSTOHFNFTITNL PYSDKAQPGTTNYQRNKR 613
DB 933 WLGSTYOLVDIHTEMESVYOPTSSSTOHFNFTITNL PYSDKAQPGTTNYQRNKR 992

QY 614 NIEDALNQLFRNSSIKSYFSDQVSTRSVPNRHHTGVDSL CNFSPILARRVDRVAIYEEF 673
DB 993 NIEDALNQLFRNSSIKSYFSDQVSTRSVPNRHHTGVDSL CNFSPILARRVDRVAIYEEF 1052

QY 674 LRMTNGTQOLNFTLDRSSVLDGYSFNRNEPPLTGN 710
DB 1053 LRMTNGTQOLNFTLDRSSVLDGYSFNRNEPPLTGN 1089

RESULT 13
US-10-198-053-479
; Sequence 479, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaityanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens

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; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-198-053-479

Query Match      92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTSPGPTVYLGASKTASIFGSAASHLLIFTLNFTTNLYEENMNG 73
DB 393 FTHRSVSTSTSPGPTVYLGASKTASIFGSAASHLLIFTLNFTTNLYEENMNG 452
QY 74 SRKFNTTERVLOGLRPLFKNTSVGPLYSGRLTLRPEKDEAGTVDALCTHRDPDGP 133
DB 453 SRKFNTTERVLOGLRPLFKNTSVGPLYSGRLTLRPEKDEAGTVDALCTHRDPDGP 512
QY 134 GUDRQLYLELSQTLHSITELGPYTLDRDSLTVNGFTHRSVPTSTGVVSEEPFLNPT 193
DB 513 GUDRQLYLELSQTLHSITELGPYTLDRDSLTVNGFTHRSVPTSTGVVSEEPFLNPT 572
QY 194 INNLRYMADMGQPSLKFNITDVMKHLISPLFORSIGARTGCRVIALRSVKNAGETR 253
DB 573 INNLRYMADMGQPSLKFNITDVMKHLISPLFORSIGARTGCRVIALRSVKNAGETR 632
QY 254 VDLCTYLOPLSGPGLPIKQVFHELSQLTHGTRIGAPYSLDKDSLTVNGNEPDPDEPT 313
DB 633 VDLCTYLOPLSGPGLPIKQVFHELSQLTHGTRIGAPYSLDKDSLTVNGNEPDPDEPT 692
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSDDMGKSAATFNSTEGVLOHLR 373
DB 693 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSDDMGKSAATFNSTEGVLOHLR 752
QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGDLIOQLYWEISQLTH 433
DB 753 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGDLIOQLYWEISQLTH 812
QY 434 GVTOLGFVYLDRLSLFINGAPONLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 493
DB 813 GVTOLGFVYLDRLSLFINGAPONLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 872
QY 494 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASH 553
DB 873 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASH 932
QY 554 WLGSTYQVLDIHTHESSVYOPTSSSTOHFLNFTTNLPYSQDAQPGTTNYORNR 613
DB 933 WLGSTYQVLDIHTHESSVYOPTSSSTOHFLNFTTNLPYSQDAQPGTTNYORNR 992
QY 614 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDRVALYEEF 673
DB 993 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDRVALYEEF 1052
QY 674 LRMTNRGTOLQNFITLDRSSVLVDGYSPPNRNEPLTGN 710
DB 1053 LRMTNRGTOLQNFITLDRSSVLVDGYSPPNRNEPLTGN 1089

RESULT 14
US-09-827-271-458
; Sequence 458, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827.271
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 458
; LENGTH: 1148
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; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-827-271-458

Query Match      92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTSPGPTVYLGASKTASIFGSAASHLLIFTLNFTTNLYEENMNG 73
DB 393 FTHRSVSTSTSPGPTVYLGASKTASIFGSAASHLLIFTLNFTTNLYEENMNG 452
QY 74 SRKFNTTERVLOGLRPLFKNTSVGPLYSGRLTLRPEKDEAGTVDALCTHRDPDGP 133
DB 453 SRKFNTTERVLOGLRPLFKNTSVGPLYSGRLTLRPEKDEAGTVDALCTHRDPDGP 512
QY 134 GUDRQLYLELSQTLHSITELGPYTLDRDSLTVNGFTHRSVPTSTGVVSEEPFLNPT 193
DB 513 GUDRQLYLELSQTLHSITELGPYTLDRDSLTVNGFTHRSVPTSTGVVSEEPFLNPT 572
QY 194 INNLRYMADMGQPSLKFNITDVMKHLISPLFORSIGARTGCRVIALRSVKNAGETR 253
DB 573 INNLRYMADMGQPSLKFNITDVMKHLISPLFORSIGARTGCRVIALRSVKNAGETR 632
QY 254 VDLCTYLOPLSGPGLPIKQVFHELSQLTHGTRIGAPYSLDKDSLTVNGNEPDPDEPT 313
DB 633 VDLCTYLOPLSGPGLPIKQVFHELSQLTHGTRIGAPYSLDKDSLTVNGNEPDPDEPT 692
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSDDMGKSAATFNSTEGVLOHLR 373
DB 693 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSDDMGKSAATFNSTEGVLOHLR 752
QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGDLIOQLYWEISQLTH 433
DB 753 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGDLIOQLYWEISQLTH 812
QY 434 GVTOLGFVYLDRLSLFINGAPONLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 493
DB 813 GVTOLGFVYLDRLSLFINGAPONLSIRGEYQINFHIVMNLSPDPTSEYITLLRDIO 872
QY 494 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASH 553
DB 873 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNASH 932
QY 554 WLGSTYQVLDIHTHESSVYOPTSSSTOHFLNFTTNLPYSQDAQPGTTNYORNR 613
DB 933 WLGSTYQVLDIHTHESSVYOPTSSSTOHFLNFTTNLPYSQDAQPGTTNYORNR 992
QY 614 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDRVALYEEF 673
DB 993 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDRVALYEEF 1052
QY 674 LRMTNRGTOLQNFITLDRSSVLVDGYSPPNRNEPLTGN 710
DB 1053 LRMTNRGTOLQNFITLDRSSVLVDGYSPPNRNEPLTGN 1089

RESULT 15
US-10-198-053-459
; Sequence 459, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 459
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-459

Query Match 92.3%; Score 3642; DB 2; Length 1156;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	14	FTHRSSVSTSTPGTPTVYLGA	SKTPASIFG	PSAASHLLIFL	TLNFTITNLRYEENMPG	73
DB	401	FTHRSSVSTSTPGTPTVYLGA	SKTPASIFG	PSAASHLLIFL	TLNFTITNLRYEENMPG	460
QY	74	SRKNTTERVLOGLRLPLFK	NTSVGLYSG	CRLLTLRPEK	GEATGVDAICTHR	133
DB	461	SRKNTTERVLOGLRLPLFK	NTSVGLYSG	CRLLTLRPEK	GEATGVDAICTHR	520
QY	134	GLDBEQLYLELSQ	LTHSITELG	PYTLDRDSL	LYNGFTHRSSVPTSTGVVSEBP	193
DB	521	GLDBEQLYLELSQ	LTHSITELG	PYTLDRDSL	LYNGFTHRSSVPTSTGVVSEBP	580
QY	194	INNLRYADMGOP	PSLKFNTIDN	VMKHLSP	LFQSSIGARYTCRVIALRSVNGAETR	253
DB	581	INNLRYADMGOP	PSLKFNTIDN	VMKHLSP	LFQSSIGARYTCRVIALRSVNGAETR	640
QY	254	VDLICTYLOPLSG	PLPIKOVF	HEL	SQQTGITRLG	313
DB	641	VDLICTYLOPLSG	PLPIKOVF	HEL	SQQTGITRLG	700
QY	314	TPKPATTEFLP	PLSATATAMG	YHLKTL	TLNFTISNLQYSPDMGKSATFNSTEGVLOHLR	373
DB	701	TPKPATTEFLP	PLSATATAMG	YHLKTL	TLNFTISNLQYSPDMGKSATFNSTEGVLOHLR	760
QY	374	PLFQKSSMGPFY	LGCCQLISLR	PEKGAATG	VDITCTYHPDPVGG	433
DB	761	PLFQKSSMGPFY	LGCCQLISLR	PEKGAATG	VDITCTYHPDPVGG	820
QY	434	GVTQLGFYVLD	RDSLFTING	YAPQNL	SIRGEYQINFHIVNNNL	493
DB	821	GVTQLGFYVLD	RDSLFTING	YAPQNL	SIRGEYQINFHIVNNNL	880
QY	494	DKYTTLYKGSQ	LHDTFRFC	LVTNLTMD	SVLVYKALFSSNLDPSLVEQVFLDKTLN	553
DB	881	DKYTTLYKGSQ	LHDTFRFC	LVTNLTMD	SVLVYKALFSSNLDPSLVEQVFLDKTLN	940
QY	554	WLGSYVQLVDI	HTEMESSY	QPTSSSTQ	HFYLNFTITNL	613
DB	941	WLGSYVQLVDI	HTEMESSY	QPTSSSTQ	HFYLNFTITNL	1000
QY	614	NIEDALNQLFR	NSIKSYFSD	CQVSTFR	SVPNRRHHTGVDSLCNFSP	673
DB	1001	NIEDALNQLFR	NSIKSYFSD	CQVSTFR	SVPNRRHHTGVDSLCNFSP	1060
QY	674	LRMTNRGTQ	QONFTLDR	SSVLVDG	YSPNRNEPLTGNS	710
DB	1061	LRMTNRGTQ	QONFTLDR	SSVLVDG	YSPNRNEPLTGNS	1097

Search completed: October 14, 2006, 04:06:07
Job time : 57 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 14, 2006, 03:55:05 ; Search time 202 Seconds
(without alignments)
1693.059 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAGPARARARTRKLFTHRSSV.....QKLISEDLMTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	748	ADS94302	AdS94302 CA 125/O7
2	3904.5	99.0	809	ADS94303	AdS94303 CA 125/O7
3	3665	92.9	6995	AEC60057	Aec60057 Human muc
4	3663	92.9	833	AA812554	Aa812554 Human ova
5	3663	92.9	833	ABP30896	Abp30896 0772P c10
6	3663	92.9	833	ADA08542	Ada08542 Human ova
7	3663	92.9	833	ADP08885	Adp08885 Secreted
8	3663	92.9	833	ADG46172	Adg46172 Human ova
9	3663	92.9	833	ADX17768	Adx17768 Human ova
10	3663	92.9	914	AA812552	Aa812552 Human ova
11	3663	92.9	914	AA899203	Aa899203 Human ova
12	3663	92.9	914	ABP30968	Abp30968 Hypotheti
13	3663	92.9	914	ABP30896	Abp30896 0772P pro
14	3663	92.9	914	ADU01425	Adu01425 Breast ca
15	3663	92.9	914	ADZ41689	Adz41689 Human bre
16	3663	92.9	914	ADA08631	Ada08631 Human o77
17	3663	92.9	914	ADA08465	Ada08465 Human ova
18	3663	92.9	914	ADP08974	Adp08974 Secreted
19	3663	92.9	914	ADP08808	Adp08808 Secreted
20	3663	92.9	914	ADG46095	Adg46095 Human ova
21	3663	92.9	914	ADN40451	Adn40451 Human bre
22	3663	92.9	914	ADX17691	Adx17691 Human ova
23	3663	92.9	914	ADX17857	Adx17857 Partial h

24	3658	92.7	1889	6	AAE34700	Aae34700 Protein e
25	3658	92.7	1890	5	ABG96381	Abg96381 Human ova
26	3658	92.7	1890	8	ADM12352	Adm12352 Human CA1
27	3658	92.7	1890	10	AEF01059	Aef01059 Ovarian c
28	3655.5	92.7	1890	8	ADO38574	Ado38574 Ovarian c
29	3651	92.5	3451	5	ABP31026	Abp31026 Amino aci
30	3651	92.5	3451	7	ADA08748	Ada08748 Human O77
31	3651	92.5	3451	7	ADP09091	Adp09091 Secreted
32	3651	92.5	3451	9	ADX17974	Adx17974 Human ova
33	3649	92.5	1148	6	ABU54692	Abu54692 Human CA1
34	3649	92.5	1148	6	ABU54693	Abu54693 Human CA1
35	3649	92.5	11721	6	ABU54721	Abu54721 Human CA1
36	3649	92.5	22157	8	ADP84155	Adp84155 Human CA1
37	3646	92.4	1148	6	ABU00145	Abu00145 Human nov
38	3642	92.3	1148	4	AA895836	Aa895836 Human pro
39	3642	92.3	1148	4	ABBS0283	Abbs0283 HOST-1 ov
40	3642	92.3	1148	5	ABG96380	Abg96380 Human ova
41	3642	92.3	1148	5	ABP30964	Abp30964 Truncated
42	3642	92.3	1148	5	ABP30969	Abp30969 Clone FLJ
43	3642	92.3	1148	7	ADA08632	Ada08632 Human O77
44	3642	92.3	1148	7	ADA08611	Ada08611 Human O77
45	3642	92.3	1148	7	ADP08954	Adp08954 Secreted

ALIGNMENTS

RESULT 1	ADS94302	standard; protein; 748 AA.
ID	ADS94302.	
XX		
AC	ADS94302.	
XX		
DT	02-DEC-2004	(first entry)
XX		
DE	CA 125/0772P 3-repeat amino acid sequence SEQ ID NO:1.	
XX		
KW	antibody; antigen-binding antibody fragment;	
KW	cell-associated CA 125/0772P; monoclonal antibody; cytostatic;	
KW	immunostimulant; mediator of lysis; tumour; cell proliferative disorder;	
KW	cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;	
KW	ovarian cancer.	
OS	Synthetic.	
XX		
PN	WO2004035537-A2.	
XX		
PD	29-APR-2004.	
XX		
PF	15-OCT-2003; 2003WO-US032945.	
XX		
PR	16-OCT-2002; 2002US-0418828P.	
PR	10-JUL-2003; 2003US-0485986P.	
XX		
PA	(EURO-) EUROCELLTQUE SA.	
PI		
XX		
PN	Albone EF, Solitis DA;	
XX		
DR	WPI; 2004-357171/33.	
XX		
PT	Novel isolated antibody, or antigen-binding antibody fragment binding	
PT	with cell-associated CA 125/0772P polypeptide relative to shed CA	
PT	125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.	
XX		
PS	Example; SEQ ID NO 1; 153bp; English.	
XX		
CC	The present invention describes an isolated antibody, or an antigen-	
CC	binding antibody fragment (I), that preferentially binds cell-associated	
CC	CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also	
CC	described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)	
CC	a monoclonal antibody that competes with binding of (II); (3) a hybridoma	
CC	as deposited in (II); (4) an isolated nucleic acid molecule (III)	
CC	comprising a nucleotide sequence that encodes a variable chain region of	

(1); (5) a pharmaceutical composition comprising an antibody or an antigen-binding antibody fragment that preferentially binds cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772P polypeptide, and a carrier; (6) a pharmaceutical composition comprising a monoclonal antibody or an antigen-binding monoclonal antibody fragment that preferentially binds cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772P polypeptide, and a carrier; (7) an article of manufacture (IV) comprising packaging material and a composition comprising an antibody, or an antigen-binding antibody fragment that preferentially binds cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772P polypeptide, and a carrier contained within the packaging material, and a composition in a form suitable for administration to a subject; (8) a fusion polypeptide (V) comprising an antibody, or an antigen-binding antibody fragment, which preferentially binds cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772P polypeptide, and a heterologous agent; (9) ameliorating (M1) a symptom of a CA 125/0772P-related disorder; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1, 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9, 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding antibody fragment; (11) an antibody or antigen binding antibody fragment that competes with (VI); and (12) a pharmaceutical composition comprising (VI) and a carrier. (I) has cytostatic activity, and can be used as an immunostimulant and a mediator of lysis of positive tumour cell. (I) is useful for ameliorating a symptom of a CA 125/077P-related disorder which is a cell proliferative disorder such as cancer, cervical or uterine cancer, breast or lung cancer or ovarian cancer. (V) is useful for cancer, breast or lung cancer or ovarian cancer. (V) is useful for cancer or tumour as part of clinical testing procedure. The present sequence represents the CA 125/0772P 3-repeat amino acid sequence, which is used in the exemplification of the present invention.

Seq Sequence 748 AA:

Query Match 100.0%; Score 3945; DB 8; Length 748;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 748; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPARARATKFTFRSSVSTSTSTGTPVYGAATPASTGSPASASHTLLFTLNFT 60
DB 1 AADPARARATKFTFRSSVSTSTSTGTPVYGAATPASTGSPASASHTLLFTLNFT 60
QY 61 ITNLRYBENWPGSRKFNTERVLOGLRPLFNNTSGVPLSGSCRLTLRPEKDGATGY 120
DB 61 ITNLRYBENWPGSRKFNTERVLOGLRPLFNNTSGVPLSGSCRLTLRPEKDGATGY 120
QY 121 DAICTHRPDPTGDLRQQLYLELSQTHSITEIGPYTLDRSLVYNGFTFRSSVPTST 180
DB 121 DAICTHRPDPTGDLRQQLYLELSQTHSITEIGPYTLDRSLVYNGFTFRSSVPTST 180
QY 181 GVUSEBPTLNFTINRLRYMADMGQPSGLKFNITDVMKHLSPRQSSLGARYGCRV 240
DB 181 GVUSEBPTLNFTINRLRYMADMGQPSGLKFNITDVMKHLSPRQSSLGARYGCRV 240
QY 241 IARSVNGAEKRVLDLCTYLOPLSGRPLIKOVFHELSQOCHGIRLGLGYSLDKSLYL 300
DB 241 IARSVNGAEKRVLDLCTYLOPLSGRPLIKOVFHELSQOCHGIRLGLGYSLDKSLYL 300
QY 301 NGYNEPDPDEPTTPKPAATFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSAT 360
DB 301 NGYNEPDPDEPTTPKPAATFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSAT 360
QY 361 FNSTEGVLQHLRPLFOKSSMGPPYLGCOILSRPEKDGATGYDTTCYHPVPGGLD 420
DB 361 FNSTEGVLQHLRPLFOKSSMGPPYLGCOILSRPEKDGATGYDTTCYHPVPGGLD 420
QY 421 IQQLYMELSQLTGVTQGLGFYVLDRLFLNGVAPQWLIRGEYQILFHVNNLSPPD 480
DB 421 IQQLYMELSQLTGVTQGLGFYVLDRLFLNGVAPQWLIRGEYQILFHVNNLSPPD 480
QY 481 TSSEYITLADIDQKVTTLTKGSQLHDTFFCULVTNLMTDSVLVTVALFSSNLDPSELV 540
DB 481 TSSEYITLADIDQKVTTLTKGSQLHDTFFCULVTNLMTDSVLVTVALFSSNLDPSELV 540

QY 541 QVFLDKTLNASEFHWLGSTYQVLDIHVTEMSSVYPTSSSSSTQHFYNFTITNLEYSQDK 600
DB 541 QVFLDKTLNASEFHWLGSTYQVLDIHVTEMSSVYPTSSSSSTQHFYNFTITNLEYSQDK 600
QY 601 AQPSTTNTQNRKRNIEDALNQLFNSSISKYSFSDCVSTFRSVPRRHITGVDSLGNFSL 660
DB 601 AQPSTTNTQNRKRNIEDALNQLFNSSISKYSFSDCVSTFRSVPRRHITGVDSLGNFSL 660
QY 661 ARVRVVAIYEFELMTNNGTQLONFPTLDRSSVLVDGYSPPNNEPLTGNADIOHSGRS 720
DB 661 ARVRVVAIYEFELMTNNGTQLONFPTLDRSSVLVDGYSPPNNEPLTGNADIOHSGRS 720
QY 721 SLEGRFPEOKLISEEDLNMTGHHHHH 748
DB 721 SLEGRFPEOKLISEEDLNMTGHHHHH 748
RESULT 2
AD594303
ID AD594303 standard; protein; 809 AA.
XX
AC AD594303;
XX
XX 02-DEC-2004 (first entry)
XX
DE CA 125/0772P 3-repeat TM amino acid sequence SEQ ID NO:2.
XX
XX antibody; antigen-binding antibody fragment;
XX cell-associated CA 125/0772P; monoclonal antibody; cytostatic;
XX immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
XX cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
XX ovarian cancer.
XX
XX Synthetic.
OS
OS WO2004035537-A2.
PN
XX 29-APR-2004.
PD
XX 15-OCT-2003; 2003MO-US032945.
PF
XX 16-OCT-2002; 2002US-0418828P.
PR 10-JUL-2003; 2003US-0485986P.
XX
XX (EURO-) EUROCELLTIGUE SA.
PA
XX Albone EF, Solits DA;
PI
XX WPI; 2004-357171/33.
DR
XX Novel isolated antibody, or antigen-binding antibody fragment binding
PT with cell-associated CA 125/0772P polypeptide relative to shed CA
PT 125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.
XX
XX Example; SEQ ID NO 2; 153pp; English.
PS
XX The present invention describes an isolated antibody, or an antigen-
XX binding antibody fragment (I), that preferentially binds cell-associated
XX CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also
XX described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
XX a monoclonal antibody that competes with binding of (II); (3) a hybridoma
XX as deposited in (II); (4) an isolated nucleic acid molecule (III)
XX comprising a nucleotide sequence that encodes a variable chain region of
XX (I); (5) a pharmaceutical composition comprising an antibody or an
XX antigen-binding antibody fragment that preferentially binds cell-
XX associated CA 125/0772P polypeptide relative to shed CA 125/0772P
XX polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
XX monoclonal antibody or an antigen-binding monoclonal antibody fragment
XX that preferentially binds cell-associated CA 125/0772P polypeptide
XX relative to shed CA 125/0772P polypeptide, and a carrier; (7) an article
XX of manufacture (IV) comprising packaging material and a composition
XX comprising an antibody, or an antigen-binding antibody fragment that
XX preferentially binds cell-associated CA 125/0772P relative to shed CA

CC 125/0772P, and a carrier contained within the packaging material, and
 CC composition in a form suitable for administration to a subject; (8) a
 CC fusion polypeptide (V) comprising an antibody, or an antigen-binding
 CC antibody fragment, which preferentially binds cell-associated CA
 CC 125/0772P relative to shed CA 125/0772P operably linked to a heterologous
 CC agent; (9) ameliorating (M1) a symptom of a CA 125/0772P-related disorder
 CC ; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 631.1, 654.1,
 CC 725.1, 869, 7F10, 8A1, 8AC3, 15C9, 8B3, 8B5, 7G10, 16C7, 7G6, 7H1, 16H9,
 CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
 CC antibody fragment; (11) an antibody or antigen binding antibody fragment
 CC that competes with (VI), and (12) a pharmaceutical composition comprising
 CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
 CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
 CC useful for ameliorating a symptom of a CA 125/077P-related disorder which
 CC is a cell proliferative disorder such as cancer, cervical or uterine
 CC cancer, breast or lung cancer or ovarian cancer. (V) is useful
 CC diagnostically for monitoring the development or progression of cancer or
 CC tumour as part of clinical testing procedure. The present sequence
 CC represents the CA 125/0772P 3-repeat TM amino acid sequence, which is
 CC used in the exemplification of the present invention.

XX Sequence 809 AA:

Query Match 99.0%; Score 3904.5; DB 8; Length 809;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 746; Conservative 0; Mismatches 0; Indels 61; Gaps 1;

QY 1 AADPARARRTKLFTHRSSVSTSTPGTPVYLCASTKPAISFGPSAASHLLILFTLNT 60
 DB 1 AADPARARRTKLFTHRSSVSTSTPGTPVYLCASTKPAISFGPSAASHLLILFTLNT 60
 QY ITNLRVENMPPGSRKNTTERTVIGLLRLFKNTSGPLYSOGRLTLLEPKGERTGV 120
 DB ITNLRVENMPPGSRKNTTERTVIGLLRLFKNTSGPLYSOGRLTLLEPKGERTGV 120
 QY 121 DALCTHRPDPYGPGLDREQLYLELSQTLSTTELGPTLDRDSLXYNGFTHRSSVPTTST 180
 DB 121 DALCTHRPDPYGPGLDREQLYLELSQTLSTTELGPTLDRDSLXYNGFTHRSSVPTTST 180
 QY 181 GVVSSEPTLNTNNLRVADMGQPSLKNITDNMKHLSPLFGRSSIGARTYTCRV 240
 DB 181 GVVSSEPTLNTNNLRVADMGQPSLKNITDNMKHLSPLFGRSSIGARTYTCRV 240
 QY 241 IALRSVNGAETRDILCTYLQPLSGPLPKQVFNHLSQOCTHGTILGPRSLDKSLYL 300
 DB 241 IALRSVNGAETRDILCTYLQPLSGPLPKQVFNHLSQOCTHGTILGPRSLDKSLYL 300
 QY 301 NGYNEPQDEPPTPKPATTFPLRLSEATTAMGVHLKTLTLNFTISNLQYSPDMGKSAT 360
 DB 301 NGYNEPQDEPPTPKPATTFPLRLSEATTAMGVHLKTLTLNFTISNLQYSPDMGKSAT 360
 QY 361 FNSTEGVLQHLRLPLFGKSSMGPFYLCQILSLRPEKOGATGVDTCTYHPPVPGGLD 420
 DB 361 FNSTEGVLQHLRLPLFGKSSMGPFYLCQILSLRPEKOGATGVDTCTYHPPVPGGLD 420
 QY 421 IQQLYMLSQLTHGVTOLGFIYLDROSLFINGAPQMLSTRGEYQINFIHVNMLSNPDP 480
 DB 421 IQQLYMLSQLTHGVTOLGFIYLDROSLFINGAPQMLSTRGEYQINFIHVNMLSNPDP 480
 QY 481 TSSSEYTLRLDIDQKVTTLKSGSLHDTFFPCVLVTNLTMOSVLTVAALFSSNLDPSLVE 540
 DB 481 TSSSEYTLRLDIDQKVTTLKSGSLHDTFFPCVLVTNLTMOSVLTVAALFSSNLDPSLVE 540
 QY 541 QVFLDKLTNLSFHWLGSYQVLVDIHVTMESSVYQPTSSSTQGFYLNFTITNLPYQDK 600
 DB 541 QVFLDKLTNLSFHWLGSYQVLVDIHVTMESSVYQPTSSSTQGFYLNFTITNLPYQDK 600
 QY 601 AOGCTTYQNRKNRIBALNQLFNSSIKSYFSCQVSTRSVNRRHHTGVDSICNFSPL 660
 DB 601 AOGCTTYQNRKNRIBALNQLFNSSIKSYFSCQVSTRSVNRRHHTGVDSICNFSPL 660
 QY 661 AARRDRVAIYEEFLMRNGTOLQNFLLDRSSVLDVGYSPNRNEPLNG----- 708
 DB 661 AARRDRVAIYEEFLMRNGTOLQNFLLDRSSVLDVGYSPNRNEPLNG----- 708

DB 661 AARRDRVAIYEEFLMRNGTOLQNFLLDRSSVLDVGYSPNRNEPLNGSDLPFWAVILI 720
 QY 709 -----NSADIQHSGR 719
 DB 721 GLAGLGLITCLICGVLVTRRRKGEYVVOQCPGYQSHLDLEDLQNSADIQHSGR 780
 QY 720 SSLEGPFEQKLISEEDLNAMHTGHHHHH 748
 DB 781 SSLEGPFEQKLISEEDLNAMHTGHHHHH 809
 RESULT 3
 AEC60057
 ID AEC60057 standard; protein; 6995 AA.
 XX AC AEC60057;
 XX DT 17-NOV-2005 (first entry)
 XX DE Human mucin 16 (MUC16).
 XX KW Receptor; tumor marker; drug delivery; drug screening; cancer;
 KW autoimmune disease; infection; Cytostatic; Antimicrobial;
 KW immunosuppressive; Antibacterial; Virostatic; Anti-HIV; Fungicide;
 KW Antiparasitic; Procoagulant; Antimalarial; Anabolic; Hypertensive;
 KW Antiarthritic; Antiallergic; Antiinflammatory; Ophthalmological;
 KW Urothelial; Dermatological.
 XX OS Homo sapiens.
 XX PN W02005081711-A2.
 XX PD 09-SEP-2005.
 XX PF 05-NOV-2004; 2004MO-US038392.
 XX PR 06-NOV-2003; 2003US-0518534P.
 XX PR 26-MAR-2004; 2004US-0557116P.
 XX PR 04-AUG-2004; 2004US-0598899P.
 XX PR 27-OCT-2004; 2004US-0622455P.
 XX PA (SEAT-) SEATTLE GENETICS INC.
 XX PI Dornina SO, Senter PD, Toki BE, Edens AJ, Kline TB, Polakis P;
 PI Sliwkowski MX, Spencer SD;
 XX DR WPI; 2005-658310/67.
 XX DR GENBANK; AAK74120.
 XX PT Novel monomethylvaline conjugate compound or its salt or solvate, useful
 PT for treating cancer, autoimmune disease and infectious disease and for
 PT diagnosing cancer.
 XX PS Disclosure; SEQ ID NO 4; 426pp; English.
 XX CC The invention relates to a monomethylvaline conjugate compound (C1) or
 CC its salt or solvate, comprising a ligand unit (particularly an antibody
 CC directed against a disease antigen) and a drug moiety (of formulae
 CC detailed in the specification). Also included are an antibody-drug
 CC conjugate compound (DC) (comprising an antibody covalently attached to
 CC one or more drug moieties), a pharmaceutical composition (PC) comprising
 CC C1 or DC, inhibiting (M1) the growth of tumor cells that overexpress a
 CC tumor-associated antigen (involves administering DC and a
 CC chemotherapeutic agent, to the patient, where DC and the chemotherapeutic
 CC agent are each administered in amounts effective to inhibit growth of
 CC tumor cells in the patient), treating a human patient susceptible to or
 CC diagnosed with a disorder characterized by overexpression of ErbB2
 CC receptor (involving administering a combination of DC and a
 CC chemotherapeutic agent), an article (AM) of manufacture comprising C1 or
 CC DC (comprising a container and a package insert or label indicating that
 CC the C1 or DC can be used to treat cancer characterized by the
 CC overexpression of at least one of CD30, CD40, CD70 and Lewis Y, or to
 CC treat cancer characterized by overexpression of an ErbB2 receptor) and

treating (M2) cancer, involves administering to a patient a formulation of DC and a diluent, carrier or excipient. In CI or DC, a substantial amount of the drug moiety is not cleaved from the antibody until CI or DC enters a cell with a cell-surface receptor specific for the antibody of CI or DC, and the drug moiety is cleaved from the antibody when CI or DC does enter the cell. The bioavailability of the compound or an intracellular metabolite of the compound in a mammal is improved when compared to a drug compound comprising the drug moiety of CI or DC. The bioavailability of the compound or an intracellular metabolite of the compound in a mammal is improved when compared to an analog of the compound not having the drug moiety. The drug moiety is intracellularly cleaved in a mammal from the antibody of CI or DC, or an intracellular metabolite of CI or DC. The antibody is at least one of AC10, S2C6, BR96, 1F6 and 2F2. In DC, the antibody specifically binds to a HER2 receptor. DC specifically binds to the extracellular domain of the HER2 receptor. DC and inhibits growth of tumor cells, which overexpress HER2 receptor. The drug conjugates are useful for killing or inhibiting the proliferation of tumor cells or cancer cells, which involves treating tumor cells or cancer cells with CP or DC, or its salt or solvate. The cancer is characterized by the overexpression of an ErbB2 receptor at a 2+ level or above. The drug conjugates are useful for treating an autoimmune disease or infectious disease, (e.g. bacterial infections caused by microorganisms such as Streptococcus pyogenes and Clostridium botulinum, viral infections caused by viruses e.g. Herpes simplex virus and HIV, fungal disease (e.g. Aspergillosis and Histoplasmosis), parasitic disease (e.g. malaria and Chagas disease), and autoimmune diseases such as Addison's disease, arthritis, allergy, Crohn's disease, Rickettsia syndrome, and systemic lupus erythematosus), all chosen from an extensive list given in the specification. The present sequence is a human tumor-associated receptor protein, antibodies against which are used in the drug conjugates of the invention.

Sequence 6995 AA;

Query Match 92.9%; Score 3665; DB 9; Length 6995;

Best Local Similarity 99.9%; Pred. No. 5, 2e-314; Indels 0; Gaps 0;

Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

14 FTHRSSVSTSTPTPTVYIGASKTSPASIFGSAASHLLILFTLNFITTLRYEENMPG 73
 6240 FTHRSSVSTSTPTPTVYIGASKTSPASIFGSAASHLLILFTLNFITTLRYEENMPG 6299
 74 SRKFNTERVLOGLRLPNTSVGLYSGCRITLRLPEKDGATGDAICTHRPPTGP 133
 6300 SRKFNTERVLOGLRLPNTSVGLYSGCRITLRLPEKDGATGDAICTHRPPTGP 6359
 134 GURBOUYELSQLTHSITELGPTLDRSLVYNGFTHRSSVPTTSNGVSEEPFLNFT 193
 6360 GURBOUYELSQLTHSITELGPTLDRSLVYNGFTHRSSVPTTSNGVSEEPFLNFT 6419
 194 INNLRVYADMGQSGSLKFNITTDVNMKHLSPFORSSIGARYTGCRVIALSVNGAETR 253
 6420 INNLRVYADMGQSGSLKFNITTDVNMKHLSPFORSSIGARYTGCRVIALSVNGAETR 6479
 254 VDLCTYLOPLSGPGLPIKOVFHELSQOTHTIRLGRYSIDKSLYANGNEGPDPBPT 313
 6480 VDLCTYLOPLSGPGLPIKOVFHELSQOTHTIRLGRYSIDKSLYANGNEGPDPBPT 6539
 314 TTPPATTFPLPLSATTAMGYHLKTLNFTISLQVSPDMGKSATFNSBEGVLOHLR 373
 6540 TTPPATTFPLPLSATTAMGYHLKTLNFTISLQVSPDMGKSATFNSBEGVLOHLR 6599
 374 PLFOKSMGPFYLCQQLISLRPEKGAATGVTCTYHPDPVGGDLIDQLYWEISQLTH 433
 6600 PLFOKSMGPFYLCQQLISLRPEKGAATGVTCTYHPDPVGGDLIDQLYWEISQLTH 6659
 434 GVTQLGFFVYLDROSLFNGTAPQWLSIRGEYOINFHIVNNLSAPPDTSSEYITLLADIQ 493
 6660 GVTQLGFFVYLDROSLFNGTAPQWLSIRGEYOINFHIVNNLSAPPDTSSEYITLLADIQ 6719
 494 DKYTLTKGSGOHTFRCVLTNLTMDSVYTVVALSSNLDPLSVGOVFLDKTLNLSFH 553
 6720 DKYTLTKGSGOHTFRCVLTNLTMDSVYTVVALSSNLDPLSVGOVFLDKTLNLSFH 6779

554 WLGSYQQLVDIHYTEMESVYOPTSSSSTQHFYINFTITNLPGSDKAQPGITMYQRNKR 613
 6780 WLGSYQQLVDIHYTEMESVYOPTSSSSTQHFYINFTITNLPGSDKAQPGITMYQRNKR 6839
 614 NIEDALNQLFNRSSIKSYFSDQVSTFRSVPNRHHTGVDSLGNFPLARRDVAIYEEF 673
 6840 NIEDALNQLFNRSSIKSYFSDQVSTFRSVPNRHHTGVDSLGNFPLARRDVAIYEEF 6899
 674 LRMTNGTQLNFTLDRSSVLVDGYSFNRNEPLTGN 710
 6900 LRMTNGTQLNFTLDRSSVLVDGYSFNRNEPLTGN 6936
 RESULT 4
 AAB12554
 ID AAB12554 standard; protein; 833 AA.
 AC AAB12554;
 XX
 XX 07-NOV-2000 (first entry)
 DT
 XX Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.
 DE
 XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
 KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN MO200036107-A2.
 XX
 PD 22-JUN-2000.
 XX
 XX 17-DEC-1999; 99WO-US030270.
 XX
 XX 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX
 XX MITcham JL, Kling GE, Algate PA, Frudakis TN;
 PI
 XX WPI; 2000-431589/37.
 DR
 XX N-PSDB; AAA70075.
 XX
 XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
 PT encoding it, useful for the diagnosis, prevention and treatment of
 PT cancer, preferably ovarian cancer.
 XX
 XX Example 2; Page 200-203; 299pp; English.
 PS
 XX The present invention describes an isolated polypeptide comprising an
 XX immunogenic portion of an ovarian carcinoma protein (or its variants).
 CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
 CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
 CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
 CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
 CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
 CC ovarian carcinoma polynucleotides and proteins used in the
 CC exemplification of the present invention
 CC
 XX
 XX Sequence 833 AA;

Query Match 92.9%; Score 3663; DB 3; Length 833;

Best Local Similarity 99.9%; Pred. No. 2, 3e-315; Indels 0; Gaps 0;

Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

14 FTHRSSVSTSTPTPTVYIGASKTSPASIFGSAASHLLILFTLNFITTLRYEENMPG 73
 78 FTHRSSVSTSTPTPTVYIGASKTSPASIFGSAASHLLILFTLNFITTLRYEENMPG 137

QY 74 SRKNTTERVLQGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 133
 DB 138 SRKNTTERVLQGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 197
 QY 134 GLDREQLYELSQLTHSITELGPTTLDRSLVYNGFTHRSVPTTSGVSEEPFLNFT 193
 DB 198 GLDREQLYELSQLTHSITELGPTTLDRSLVYNGFTHRSVPTTSGVSEEPFLNFT 257
 QY 194 INNLRYADMGGQPSLKFENITDVMKHLSPFORSSLGARYGCRVIALRSYNGAETR 253
 DB 258 INNLRYADMGGQPSLKFENITDVMKHLSPFORSSLGARYGCRVIALRSYNGAETR 317
 QY 254 VDLCTYLOPLSGPGLPIKQVPHLSQOTGTRIGSYSDKXSLVYNGNEGPDPPT 313
 DB 318 VDLCTYLOPLSGPGLPIKQVPHLSQOTGTRIGSYSDKXSLVYNGNEGPDPPT 377
 QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
 DB 378 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLOHLR 437
 QY 374 PLFOKSMGPFFYLGCQLISLRPEKDGATGVDITCTHDPVPGGLDIQOLYWEISQLTH 433
 DB 438 PLFOKSMGPFFYLGCQLISLRPEKDGATGVDITCTHDPVPGGLDIQOLYWEISQLTH 497
 QY 434 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYOINFHIVMNLSPDPTSEYITLLRDIO 493
 DB 498 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYOINFHIVMNLSPDPTSEYITLLRDIO 557
 QY 494 DKVTLTYKGSQDLHDFRFLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASH 553
 DB 558 DKVTLTYKGSQDLHDFRFLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASH 617
 QY 554 WLGSYQVLDIHTVEMESSYQPTSSSTQHFLNFTTNLPYSODKAPGTTNYQRNKR 613
 DB 618 WLGSYQVLDIHTVEMESSYQPTSSSTQHFLNFTTNLPYSODKAPGTTNYQRNKR 677
 QY 614 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSLGNFSLARRVDVAIYEER 673
 DB 678 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSLGNFSLARRVDVAIYEER 737
 QY 674 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 710
 DB 738 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 774

RESULT 5
 ABB30898
 ID ABB30898 standard; protein; 833 AA.
 XX
 AC ABB30898;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE 0772P clone 21003.
 XX
 KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN MO200206317-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001MO-US022635.
 XX
 PR 17-JUL-2000; 2000US-00617747.
 XX
 PR 10-AUG-2000; 2000US-00636801.
 XX
 PR 20-SEP-2000; 2000US-00667857.
 XX
 PR 04-APR-2001; 2001US-00827171.
 XX
 PR 18-JUN-2001; 2001US-00884441.
 XX
 PA (CORI-) CORIXA CORP.
 XX

PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
 PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 DR WPI; 2002-164781/21.
 DR N-PSDB; ABN72969.
 XX
 PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
 PT protein or its variants, useful for stimulating an immune response in a
 PT patient and treating ovarian cancer.
 XX
 PS Example 2; Page 316-318; 408pp; English.
 XX
 CC This invention relates to polypeptides comprising an immunogenic portion
 CC of an ovarian carcinoma protein which access an immunostimulant and is
 CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations and antigen presenting cells that express
 CC the polypeptides are useful for stimulating an immune response in a
 CC patient and treating ovarian cancer. This sequence represents protein
 CC related to the invention
 XX
 SQ Sequence 833 AA;
 XX
 Query Match 92.9%; Score 3663; DB 5; Length 833;
 Best local Similarity 99.9%; Pred. No. 2,3e-315;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 14 FTHRSSVSTSTTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTTNLRYEENMWG 73
 DB 78 FTHRSSVSTSTTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTTNLRYEENMWG 137
 QY 74 SRKNTTERVLQGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 133
 DB 138 SRKNTTERVLQGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 197
 QY 134 GLDREQLYELSQLTHSITELGPTTLDRSLVYNGFTHRSVPTTSGVSEEPFLNFT 193
 DB 198 GLDREQLYELSQLTHSITELGPTTLDRSLVYNGFTHRSVPTTSGVSEEPFLNFT 257
 QY 194 INNLRYADMGGQPSLKFENITDVMKHLSPFORSSLGARYGCRVIALRSYNGAETR 253
 DB 258 INNLRYADMGGQPSLKFENITDVMKHLSPFORSSLGARYGCRVIALRSYNGAETR 317
 QY 254 VDLCTYLOPLSGPGLPIKQVPHLSQOTGTRIGSYSDKXSLVYNGNEGPDPPT 313
 DB 318 VDLCTYLOPLSGPGLPIKQVPHLSQOTGTRIGSYSDKXSLVYNGNEGPDPPT 377
 QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
 DB 378 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLOHLR 437
 QY 374 PLFOKSMGPFFYLGCQLISLRPEKDGATGVDITCTHDPVPGGLDIQOLYWEISQLTH 433
 DB 438 PLFOKSMGPFFYLGCQLISLRPEKDGATGVDITCTHDPVPGGLDIQOLYWEISQLTH 497
 QY 434 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYOINFHIVMNLSPDPTSEYITLLRDIO 493
 DB 498 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYOINFHIVMNLSPDPTSEYITLLRDIO 557
 QY 494 DKVTLTYKGSQDLHDFRFLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASH 553
 DB 558 DKVTLTYKGSQDLHDFRFLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASH 617
 QY 554 WLGSYQVLDIHTVEMESSYQPTSSSTQHFLNFTTNLPYSODKAPGTTNYQRNKR 613
 DB 618 WLGSYQVLDIHTVEMESSYQPTSSSTQHFLNFTTNLPYSODKAPGTTNYQRNKR 677
 QY 614 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSLGNFSLARRVDVAIYEER 673
 DB 678 NIEDALNQLFRNSSISYFSDCOVSTFRSVPNRHHTGVDSLGNFSLARRVDVAIYEER 737
 QY 674 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 710
 DB 738 LRMTNGTOLQNFLLDRSSVLYDGYSPNRNEPLTGN 774

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RESULT 6
ADA08542
ID ADA08542 standard; protein; 833 AA.
XX
AC ADA08542;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma antigen O772P #2.
XX
KW human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2003-532352/50.
XX
PT New isolated O772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
PS Example 2; SEQ ID NO 389; 371bp; English.
XX
CC The invention relates to an isolated O772P polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen.
XX
SQ Sequence 833 AA;
XX
Query Match 92.9%; Score 3663; DB 7; Length 833;
Best Local Similarity 99.9%; Pred. No. 2,36-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 14 FTHRSSYSTSTPTPTVYLGASKTPTASIFGPSAASHLLIFLTNFTITNLRKYENMPG 73
DB 78 FTHRSSVYSTSTPTPTVYLGASKTPTASIFGPSAASHLLIFLTNFTITNLRKYENMPG 137
OY 74 SRKNTTERVYQGLRPLFKNTSVGPLYSGRLTLRLPEKDGKATGVDAICTHRPDPGP 133
DB 138 SRKNTTERVYQGLRPLFKNTSVGPLYSGRLTLRLPEKDGKATGVDAICTHRPDPGP 197
OY 134 GLDREQLYLELSQLTHTSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVSEEPFTLNFT 193

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DB 198 GLDREQLYLELSQLTHTSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVSEEPFTLNFT 257
OY 194 INNLRVADMGQSGSLKFNITTDNMKHLSPLFORSISGARVYGCRIYALRSVNGAETR 253
DB 258 INNLRVADMGQSGSLKFNITTDNMKHLSPLFORSISGARVYGCRIYALRSVNGAETR 317
OY 254 VDLICTYLOPLSGPGLPIKQVFNHLSQOHTGITRLGFPYSLDKDSLUNGYNPEGPDPPT 313
DB 318 VDLICTYLOPLSGPGLPIKQVFNHLSQOHTGITRLGFPYSLDKDSLUNGYNPEGPDPPT 377
OY 314 TPKPATTFELPPLSEATTAMGYHKLTLTNFTISNLQVSPDMKGSATFTNTEGVLQHLLR 373
DB 378 TPKPATTFELPPLSEATTAMGYHKLTLTNFTISNLQVSPDMKGSATFTNTEGVLQHLLR 437
OY 374 PLFQKSSMGPPYLCCQLISLRPEKDGATGVDTCTHPPDPVPGGLDIQQLYMLSQLTHT 433
DB 438 PLFQKSSMGPPYLCCQLISLRPEKDGATGVDTCTHPPDPVPGGLDIQQLYMLSQLTHT 497
OY 434 GVTOLGFPYVLDRLSLFINGVAPONLSIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIQ 493
DB 498 GVTOLGFPYVLDRLSLFINGVAPONLSIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIQ 557
OY 494 DKVTTLYKGSQLDHTFRFCVLTNLTMDSVLYTVYKALFESNLDPSLYEGVFLDKTLNASFH 553
DB 558 DKVTTLYKGSQLDHTFRFCVLTNLTMDSVLYTVYKALFESNLDPSLYEGVFLDKTLNASFH 617
OY 554 WLGSTYQVLDIHVTEMESVYOPTSSSTQHPFYNFTTNLPYSODKAQPGTTYQNRKR 613
DB 618 WLGSTYQVLDIHVTEMESVYOPTSSSTQHPFYNFTTNLPYSODKAQPGTTYQNRKR 677
OY 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSVPRHHTGVDSLGNFGLARRVDRVAIYEEF 673
DB 678 NIEDALNQLFRNSIKSYFSDCOVSTFRSVPRHHTGVDSLGNFGLARRVDRVAIYEEF 737
OY 674 LRMTRNGTQLQNFLLDRSSVLVDGYSFPRNREPLTNS 710
DB 738 LRMTRNGTQLQNFLLDRSSVLVDGYSFPRNREPLTNS 774
RESULT 7
ADF08885
ID ADF08885 standard; protein; 833 AA.
XX
AC ADF08885;
XX
DT 12-FEB-2004 (first entry)
XX
DE Secreted ovarian carcinoma antigen seq'd 389.
XX
KW gene therapy; protein therapy; vaccine; antibody inhibition;
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
KW secreted ovarian carcinoma antigen.
XX
OS Homo sapiens.
XX
PN US2003124140-A1.
XX
PD 03-JUL-2003.
XX
PF 17-JUL-2002; 2002US-00198053.
XX
PR 17-DEC-1998; 98US-00215681.
XX
PR 17-DEC-1998; 98US-00216003.
XX
PR 23-JUN-1999; 99US-00338933.
XX
PR 24-SEP-1999; 99US-00404879.
XX
PR 17-JUL-2000; 2000US-00617747.
XX
PR 10-AUG-2000; 2000US-00636801.
XX
PR 20-SEP-2000; 2000US-0067857.
XX
PR 04-APR-2001; 2001US-00827271.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PR 17-JUL-2001; 2001US-00907969.
XX
PA (CORI-) CORIXA CORP.

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XX Bangur GS, Retter MM, Fanger GR, Hill P;
PI WPI; 2003-897152/82.
XX N-PSDB; ADF08882.
DR
XX
PT Oncogenic nucleic acids useful for the prevention, diagnosis and
treatment of breast cancer.
XX
XX Example 2; SEQ ID NO 389; 399pp; English.
XX
CC The invention describes nucleic acids (I) and the polypeptides (II) they
CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
CC treating diseases related to their aberrant expression i.e. breast
CC cancers. For example, (I) and (II) may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of (II) by expressing
CC inactive proteins or to supplement the patient's own production of (II).
CC Additionally, (I) may be used to produce (II), by inserting (I) into a
CC host cell and culturing the cell to express the protein (II). (I) And its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids in
CC samples, and therefore which patients may be in need of restorative
CC therapy. The host cell may also be used as antigens in the production of
CC antibodies against (II) and in assays to identify modulators of (II)'s
CC expression and activity. The anti-(II) antibodies, agonists and
CC antagonists may be used to regulate expression and activity and as
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
CC immunoassay). This sequence represents a secreted ovarian carcinoma
CC antigen.
XX
XX Sequence 833 AA;
SQ
Query Match 92.9%; Score 3663; DB 7; Length 833;
Best Local Similarity 99.9%; Pred. No. 2.3e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPTGTPVYVIGASTPTASIFGPSASHLLILFTINFTINLRBYENMWPG 73
DB 78 FTHRSSVSTSTPTGTPVYVIGASTPTASIFGPSASHLLILFTINFTINLRBYENMWPG 137
QY 74 SRKFNTERVLOGLRPLFKNTSGVPLYSGCRLTLRPEKGEATGVDAICTHRPDPTGP 133
DB 138 SRKFNTERVLOGLRPLFKNTSGVPLYSGCRLTLRPEKGEATGVDAICTHRPDPTGP 197
QY 134 GLDREQLYLELSQTLHSITELGPTLDRDSLNVNGFTHRSSVPTSTGVSEEPFTINFT 193
DB 198 GLDREQLYLELSQTLHSITELGPTLDRDSLNVNGFTHRSSVPTSTGVSEEPFTINFT 257
QY 194 INNLRVADMGQPGSLKFNITDVMKILSPLFORSSLGARYTGCRIYALRSVNGAETR 253
DB 258 INNLRVADMGQPGSLKFNITDVMKILSPLFORSSLGARYTGCRIYALRSVNGAETR 317
QY 254 VDLICTYLOPLSGRGLPIKOVFHELSQOHTGIRLGYSLDKOSLYINGNEGPDPPT 313
DB 318 VDLICTYLOPLSGRGLPIKOVFHELSQOHTGIRLGYSLDKOSLYINGNEGPDPPT 377
QY 314 TPKPATFTPLSEATTAMGVHLKTLINFTISNLQYSPMGKGSATFNSTEGVLQHLR 373
DB 378 TPKPATFTPLSEATTAMGVHLKTLINFTISNLQYSPMGKGSATFNSTEGVLQHLR 437
QY 374 PLFOKSSMGPFYIGCOLISLRPEKGAATGVDITCTYHPDPVGGDLIDQLYWEISQTLH 433
DB 438 PLFOKSSMGPFYIGCOLISLRPEKGAATGVDITCTYHPDPVGGDLIDQLYWEISQTLH 497
QY 434 GVTOLGTYVLDRLSLFNGYAPOMLSIRGEYQINFNHVMNNLSNPDPSTSEYITLLRDIO 493
DB 498 GVTOLGTYVLDRLSLFNGYAPOMLSIRGEYQINFNHVMNNLSNPDPSTSEYITLLRDIO 557
QY 494 DKYTTLYKGSQLDHDFRCLVTNLTMDSVLYVYKALFPSSNIDPSLVEQVLDLKTINASFH 553
DB 558 DKYTTLYKGSQLDHDFRCLVTNLTMDSVLYVYKALFPSSNIDPSLVEQVLDLKTINASFH 617

QY 554 WLGSTYOLVDIHTEMESSYOPTSSSSSTOHFYLFNTITNLPSYODKAPGPTNYORNR 613
DB 618 WLGSTYOLVDIHTEMESSYOPTSSSSSTOHFYLFNTITNLPSYODKAPGPTNYORNR 677
QY 614 NIEDALNOLFNRNSISYFSDCCVSTFRSVNHRHTGVDSLGNFSPLARRDVAIYEAF 673
DB 678 NIEDALNOLFNRNSISYFSDCCVSTFRSVNHRHTGVDSLGNFSPLARRDVAIYEAF 737
QY 674 LRMTNRGTQLQNTLDRSSVLDVGYSPNRPPLTNGS 710
DB 738 LRMTNRGTQLQNTLDRSSVLDVGYSPNRPPLTNGS 774
RESULT 8
ADG46172
ID ADG46172 standard; protein; 833 AA.
XX
AC ADG46172;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human ovarian carcinoma polypeptide #3.
XX
KM Human; ovarian carcinoma; OBE; ovarian cancer; secreted tumour antigen;
KW Cytostatic; O772P.
XX
OS Homo sapiens.
XX
PN US2003165504-A1.
XX
PD 04-SEP-2003.
XX
PF 04-APR-2001; 2001US-00827271.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
XX
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
XX
PI Retter MM, Fanger GR;
XX
DR WPI; 2003-898035/82.
XX
PT New isolated OBE or O772P polypeptides, useful for diagnosing,
PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
PT stimulating the immune response in patient.
XX
PS Claim 5; SEQ ID NO 389; 290pp; English.
XX
XX
CC The invention relates to human ovarian carcinoma polypeptides, designated
CC OBE or O772P, and the polynucleotides encoding them. The invention also
CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polypeptide of the invention.
XX
SQ Sequence 833 AA;
Query Match 92.9%; Score 3663; DB 7; Length 833;
Best Local Similarity 99.9%; Pred. No. 2.3e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPTGTPVYVIGASTPTASIFGPSASHLLILFTINFTINLRBYENMWPG 73

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Db      78 FTHRSSVSTSTPGPTVYLGAASKTPASIFGPSAASHLLILFTLNFTINLRYEENMMPG 137
Qy      74 SRKFNTTTERVLOQLRLPLFKNTSVGPLYSGCRLLTLRPRKDEAGVDAICTHRDPDTPG 133
Db      138 SRKFNTTTERVLOQLRLPLFKNTSVGPLYSGCRLLTLRPRKDEAGVDAICTHRDPDTPG 197
Qy      134 GIDREOLYELSQLTHSITELGPTLDRDSLVLNGGTHSSVPTTSTGVVSEEPFLNFT 193
Db      198 GIDREOLYELSQLTHSITELGPTLDRDSLVLNGGTHSSVPTTSTGVVSEEPFLNFT 257
Qy      194 INNLRYMADMGQPGSLKFNITDVMGHLLSPLEFORSSLGARYTGCVIALRSYKNGAETR 253
Db      258 INNLRYMADMGQPGSLKFNITDVMGHLLSPLEFORSSLGARYTGCVIALRSYKNGAETR 317
Qy      254 VDLCTYLOPLSGPGLPIKQVFHELSQOTHGTRLRGPLYSDKDSLVLNGYNEGPDEPPT 313
Db      318 VDLCTYLOPLSGPGLPIKQVFHELSQOTHGTRLRGPLYSDKDSLVLNGYNEGPDEPPT 377
Qy      314 TRKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKSGATFNSSTEGVLOHLR 373
Db      378 TRKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKSGATFNSSTEGVLOHLR 437
Qy      374 PLFOKSSMGPFYLGCOLISLRPKDGAAGVDTCTYHDPVPGGLDIQOLYELSQLTH 433
Db      438 PLFOKSSMGPFYLGCOLISLRPKDGAAGVDTCTYHDPVPGGLDIQOLYELSQLTH 497
Qy      434 GVTQLGFYVLDRLDSLFLNGYAPONLSIRGEYQINFHIVMNLNPDPTSEYITLLRDIO 493
Db      498 GVTQLGFYVLDRLDSLFLNGYAPONLSIRGEYQINFHIVMNLNPDPTSEYITLLRDIO 557
Qy      494 DKYTTLYKGSQQLHDTFRFCLVNTLMDSVLVYTKALFSSNLDPSLVEQVFLDKTLNASHF 553
Db      558 DKYTTLYKGSQQLHDTFRFCLVNTLMDSVLVYTKALFSSNLDPSLVEQVFLDKTLNASHF 617
Qy      554 WLGSTYQLVDIHTEMESSYQOPTSSSTQHFYLNFTITNLPSODKAOPGTNNYQRNKR 613
Db      618 WLGSTYQLVDIHTEMESSYQOPTSSSTQHFYLNFTITNLPSODKAOPGTNNYQRNKR 677
Qy      614 NIEDALNQLFRNSSIKSYFSDCCVSTFRSVPNRHHTGVDSLGNFSPLARRDVAIYEER 673
Db      678 NIEDALNQLFRNSSIKSYFSDCCVSTFRSVPNRHHTGVDSLGNFSPLARRDVAIYEER 737
Qy      674 LRMTNRGTQLONTFLDRSSVLVDGYSPNNRNEPLTGNS 710
Db      738 LRMTNRGTQLONTFLDRSSVLVDGYSPNNRNEPLTGNS 774

RESULT 9
ADX17768
ID      ADX17768 standard; protein; 833 AA.
AC      ADX17768;
XX
DT      21-APR-2005 (first entry)
XX
DE      Human ovarian carcinoma antigen cDNA O772P clone 21003 encoded protein.
XX
KW      diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
KM      ovarian tumor; cancer; carcinoma; antigen.
OS      Homo sapiens.
XX
XX      US2005031634-A1.
PN      10-FEB-2005.
PD
XX
PF      02-JUN-2004; 2004US-00860790.
XX
PR      17-DEC-1998; 98US-00216003.
PR      23-JUN-1999; 99US-00338933.
PR      24-SEP-1999; 99US-00404879.
PR      17-JUL-2000; 2000US-00617747.

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PR      10-AUG-2000; 2000US-00636801.
PR      20-SEP-2000; 2000US-00667857.
PR      04-APR-2001; 2001US-00827271.
PR      18-JUN-2001; 2001US-00884441.
PR      17-JUL-2001; 2001US-00907969.
PR      17-JUL-2002; 2002US-00198053.
XX
PA      (CORI-) CORIXA CORP.
XX
XX      Bangur CS, Rector MW, Fanger GR, Hill P;
PI      WPI; 2005-151645/16.
XX
DR      New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT      diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT      for eliciting humoral and/or cellular immune response.
XX
XX      Example 2; SEQ ID NO 389; 398bp; English.
XX
XX      The invention relates to an isolated polynucleotide comprising a sequence
CC      of, a sequence hybridizing under highly stringent conditions to, or
CC      having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC      the specification, its complement or degenerate variants, or a sequence
CC      of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC      polynucleotides and polypeptides are useful for diagnosing, preventing
CC      and treating diseases, such as ovarian cancer, and for eliciting humoral
CC      and/or cellular immune response. This sequence corresponds to an ovarian
CC      carcinoma antigen protein of the invention.
XX
XX      Sequence 833 AA;
SQ

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Query Match      92.9%; Score 3663; DB 9; Length 833;
Best Local Similarity 99.9%; Pred. No. 2,3e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      14 FTHRSSVSTSTPGPTVYLGAASKTPASIFGPSAASHLLILFTLNFTINLRYEENMMPG 73
Db      78 FTHRSSVSTSTPGPTVYLGAASKTPASIFGPSAASHLLILFTLNFTINLRYEENMMPG 137
Qy      74 SRKFNTTTERVLOQLRLPLFKNTSVGPLYSGCRLLTLRPRKDEAGVDAICTHRDPDTPG 133
Db      138 SRKFNTTTERVLOQLRLPLFKNTSVGPLYSGCRLLTLRPRKDEAGVDAICTHRDPDTPG 197
Qy      134 GIDREOLYELSQLTHSITELGPTLDRDSLVLNGGTHSSVPTTSTGVVSEEPFLNFT 193
Db      198 GIDREOLYELSQLTHSITELGPTLDRDSLVLNGGTHSSVPTTSTGVVSEEPFLNFT 257
Qy      194 INNLRYMADMGQPGSLKFNITDVMGHLLSPLEFORSSLGARYTGCVIALRSYKNGAETR 253
Db      258 INNLRYMADMGQPGSLKFNITDVMGHLLSPLEFORSSLGARYTGCVIALRSYKNGAETR 317
Qy      254 VDLCTYLOPLSGPGLPIKQVFHELSQOTHGTRLRGPLYSDKDSLVLNGYNEGPDEPPT 313
Db      318 VDLCTYLOPLSGPGLPIKQVFHELSQOTHGTRLRGPLYSDKDSLVLNGYNEGPDEPPT 377
Qy      314 TRKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKSGATFNSSTEGVLOHLR 373
Db      378 TRKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKSGATFNSSTEGVLOHLR 437
Qy      374 PLFOKSSMGPFYLGCOLISLRPKDGAAGVDTCTYHDPVPGGLDIQOLYELSQLTH 433
Db      438 PLFOKSSMGPFYLGCOLISLRPKDGAAGVDTCTYHDPVPGGLDIQOLYELSQLTH 497
Qy      434 GVTQLGFYVLDRLDSLFLNGYAPONLSIRGEYQINFHIVMNLNPDPTSEYITLLRDIO 493
Db      498 GVTQLGFYVLDRLDSLFLNGYAPONLSIRGEYQINFHIVMNLNPDPTSEYITLLRDIO 557
Qy      494 DKYTTLYKGSQQLHDTFRFCLVNTLMDSVLVYTKALFSSNLDPSLVEQVFLDKTLNASHF 553
Db      558 DKYTTLYKGSQQLHDTFRFCLVNTLMDSVLVYTKALFSSNLDPSLVEQVFLDKTLNASHF 617
Qy      554 WLGSTYQLVDIHTEMESSYQOPTSSSTQHFYLNFTITNLPSODKAOPGTNNYQRNKR 613

```

Db 618 WLGSYQLVDIHVTEMESSVYOPTSSSTQHFLNFTITNLPSQDKAOPGTTNYQNRK 677

QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHGVDSLGNFSPILARRVDAIYEER 673

Db 678 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHGVDSLGNFSPILARRVDAIYEER 737

QY 674 LRMTNGTQLQNFLLDRSSVLDGYSPPNRNEPLTGN 710

Db 738 LRMTNGTQLQNFLLDRSSVLDGYSPPNRNEPLTGN 774

RESULT 10

AA12552

ID AA12552 standard; protein; 914 AA.

XX AA12552;

AC

DT 07-NOV-2000 (first entry)

XX

DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.

XX

KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;

OS tumour antigen; identification; cytosolic; gene therapy; vaccine.

XX Homo sapiens.

PN MO200036107-A2.

XX

PD 22-JUN-2000.

XX

PF 17-DEC-1999; 99MO-US030270.

XX

PR 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.

XX

PA (CORI-) CORIXA CORP.

PI Mitcham JL, King GE, Aigate PA, Frudakis TN;

XX

DR WPI; 2000-41589/37.

DR N-PSDB; AAAT0001.

XX

PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid

PT encoding it, useful for the diagnosis, prevention and treatment of

PT cancer, preferably ovarian cancer.

XX

PS Example 2; Page 172-174; 299pp; English.

XX

CC The present invention describes an isolated polypeptide comprising an

CC immunogenic portion of an ovarian carcinoma protein (or its variants).

CC Ovarian carcinoma proteins, and polynucleotides encoding them, have

CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian

CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful

CC for the prevention, diagnosis and treatment of cancer, preferably ovarian

CC cancer. AA69691 to AA7007 and AA12552 to AA12557 represent human

CC ovarian carcinoma polynucleotides and proteins used in the

CC exemplification of the present invention

XX

SO Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 3; Length 914;

Best Local Similarity 99.9%; Pred. No. 2,7e-315;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTGCTPTVYIGAKTPASTGSPASASHLLTLFLNFTITNLRYEENMWG 73

Db 159 FTHRSSVSTSTGCTPTVYIGAKTPASTGSPASASHLLTLFLNFTITNLRYEENMWG 218

QY 74 SRKFTTERVLOGILRLPLFKNTSVGPYSGRLTLRLPEKGGATGVAICTHRPDPGP 133

Db 219 SRKFTTERVLOGILRLPLFKNTSVGPYSGRLTLRLPEKGGATGVAICTHRPDPGP 278

QY 134 GLDREQLYLELSQITHELAPYTLDRDSL YNNGFTHRSSVPTTSAGVSEEPPTLNFT 193

Db 279 GLDREQLYLELSQITHELAPYTLDRDSL YNNGFTHRSSVPTTSAGVSEEPPTLNFT 338

QY 194 INNLRYMADMGQSGSLKFNITDNVMGHLSPLEORSLSGARVYGCIVIALRSYKGAETR 253

Db 339 INNLRYMADMGQSGSLKFNITDNVMGHLSPLEORSLSGARVYGCIVIALRSYKGAETR 398

QY 254 VDLCTYLOPLSGPGPLIKQVFHELSQOHTGTRLCAPYSLDKSLYLNGNEGPDPPT 313

Db 399 VDLCTYLOPLSGPGPLIKQVFHELSQOHTGTRLCAPYSLDKSLYLNGNEGPDPPT 458

QY 314 TPKPATPLPLSEATAMGYHLKTLTLNFTSNLOYSPPMGKGSATFNSTEGVLOHLR 373

Db 459 TPKPATPLPLSEATAMGYHLKTLTLNFTSNLOYSPPMGKGSATFNSTEGVLOHLR 518

QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCYHPDPVGPGLDIQOLYWELSQLT 433

Db 519 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCYHPDPVGPGLDIQOLYWELSQLT 578

QY 434 GVTQLGFVYLDRLDSLFINGVAPQNLISGEYQINPHIYVMNLSNPDPTSSEYITLLRDIO 493

Db 579 GVTQLGFVYLDRLDSLFINGVAPQNLISGEYQINPHIYVMNLSNPDPTSSEYITLLRDIO 638

QY 494 DKVTTLKSGSLQHDTRFCLVNTLMDSVLVYVKALFSSNLDPSLYEQLDXTLNASH 553

Db 639 DKVTTLKSGSLQHDTRFCLVNTLMDSVLVYVKALFSSNLDPSLYEQLDXTLNASH 698

QY 554 WLGSYQLVDIHVTEMESSVYOPTSSSTQHFLNFTITNLPSQDKAOPGTTNYQNRK 613

Db 699 WLGSYQLVDIHVTEMESSVYOPTSSSTQHFLNFTITNLPSQDKAOPGTTNYQNRK 758

QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHGVDSLGNFSPILARRVDAIYEER 673

Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHGVDSLGNFSPILARRVDAIYEER 818

QY 674 LRMTNGTQLQNFLLDRSSVLDGYSPPNRNEPLTGN 710

Db 819 LRMTNGTQLQNFLLDRSSVLDGYSPPNRNEPLTGN 855

RESULT 11

AA12552

ID AA12552 standard; protein; 914 AA.

XX AA12552;

AC

DT 04-SEP-2001 (first entry)

XX

DE Human ovarian tumour-derived antigen O772P.

XX

KW Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;

OS antigen; O772P.

XX

OS Homo sapiens.

XX

PN MO200140269-A2.

XX

PD 07-JUN-2001.

XX

PF 29-NOV-2000; 2000MO-US032520.

XX

PR 30-NOV-1999; 99US-00451651.

PR 22-FEB-2000; 2000US-00510662.

PR 10-MAR-2000; 2000US-00523586.

PR 07-APR-2000; 2000US-00545068.

PR 15-MAY-2000; 2000US-00571025.

XX

PA (CORI-) CORIXA CORP.

PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;

DR WPI; 2001-356154/37.
DR N-PSDB; AAH55680.

XX Breast tumor polypeptides and the nucleic acids that encode them, useful
PT for the prevention, diagnosis and treatment of breast cancer.

XX Example 3; Page 187-188; 221pp; English.

XX The present invention relates to human breast tumour protein coding
CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
CC AAH55762). The breast tumour protein DNA sequences may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the breast tumour protein e.g. breast cancer.
CC The present sequence is a human ovarian tumour-derived antigen, which was
CC used in an example from the present invention

XX Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 2,7e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 14 FTHRSVSTSTSTGPTTVVVGASKTPASIFGPAASHLLILFTLNTTINLRYEENMMPG 73
DB 159 FTHRSVSTSTSTGPTTVVVGASKTPASIFGPAASHLLILFTLNTTINLRYEENMMPG 218
QY 74 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPPTGP 133
DB 219 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPPTGP 278
QY 134 GDRBOLYLIELSOLTHSITELEGPYTLDRDSLVLNNGFTHRSVPTTSTGVVSEBPTLNT 193
DB 279 GDRBOLYLIELSOLTHSITELEGPYTLDRDSLVLNNGFTHRSVPTTSTGVVSEBPTLNT 338
QY 194 INNLRYADMGOGSLKFNITDVMVKHLSPFORSLGARVYGCRIYALRSYNGAETR 253
DB 339 INNLRYADMGOGSLKFNITDVMVKHLSPFORSLGARVYGCRIYALRSYNGAETR 398
QY 254 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGIRLGPYSIDKDSLVLNNGNEBGPDEPPT 313
DB 399 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGIRLGPYSIDKDSLVLNNGNEBGPDEPPT 458
QY 314 TPKPATTFLPPLSBATTAMGYHLKTLTNTISNLQYSPMGKGSATFNSTEGVLOHLR 373
DB 459 TPKPATTFLPPLSBATTAMGYHLKTLTNTISNLQYSPMGKGSATFNSTEGVLOHLR 518
QY 374 PLFOKSMGPFYIGCOLISLRPEKDAATGVDTCTYHPDVGGLDIQOLYIELSOLTH 433
DB 519 PLFOKSMGPFYIGCOLISLRPEKDAATGVDTCTYHPDVGGLDIQOLYIELSOLTH 578
QY 434 GVTOLGYVLDRLDLFINGYAPQNLIRGEYQINFHIVNNLSNPDTSESSEYITLLRDIO 493
DB 579 GVTOLGYVLDRLDLFINGYAPQNLIRGEYQINFHIVNNLSNPDTSESSEYITLLRDIO 638
QY 494 DKVTTLVKGSGLDHDTFFRCVLTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNLSFH 553
DB 639 DKVTTLVKGSGLDHDTFFRCVLTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNLSFH 698
QY 554 WLGSYLOLVDIHTWEMSSVYQPTSSSTQHFYINFTITNLRYQODKAOQPTMYQNRKR 613
DB 699 WLGSYLOLVDIHTWEMSSVYQPTSSSTQHFYINFTITNLRYQODKAOQPTMYQNRKR 758
QY 614 NIEBALNOLFNSSISKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSLARVDRVAIYEEF 673
DB 759 NIEBALNOLFNSSISKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSLARVDRVAIYEEF 818
QY 674 LRMTNRTQLONFLDSSSVLVDSYSPNRNBPPLTGN 710
DB 819 LRMTNRTQLONFLDSSSVLVDSYSPNRNBPPLTGN 855

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RESULT 12
ABP30968

ID ABP30968 standard; protein; 914 AA.

XX AC ABP30968;

XX DT 02-JUN-2002 (first entry)

XX DE Hypothetical protein sequence for clone 0772P.

XX KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.

XX OS Homo sapiens.

XX PN WO200206317-A2.

XX PD 24-JAN-2002.

XX PF 17-JUN-2001; 2001WO-US022635.

XX PR 17-JUN-2000; 2000US-00617747.

XX PR 10-AUG-2000; 2000US-00636801.

XX PR 20-SEP-2000; 2000US-00667857.

XX PR 04-APR-2001; 2001US-00827271.

XX PR 18-JUN-2001; 2001US-00884441.

XX PA (CORI-) CORIXA CORP.

XX PI Mitcham JU, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,

XX PI Reed SG, Vedvick TS, Carter D, Hill F, Albone E;

XX DR WPI; 2002-164781/21.

XX DR N-PSDB; ABN72974.

XX PS Disclosure; Page 350-352; 408pp; English.

XX This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytotoxic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention

XX Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 5; Length 914;
Best Local Similarity 99.9%; Pred. No. 2,7e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 14 FTHRSVSTSTSTGPTTVVVGASKTPASIFGPAASHLLILFTLNTTINLRYEENMMPG 73
DB 159 FTHRSVSTSTSTGPTTVVVGASKTPASIFGPAASHLLILFTLNTTINLRYEENMMPG 218
QY 74 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPPTGP 133
DB 219 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPPTGP 278
QY 134 GDRBOLYLIELSOLTHSITELEGPYTLDRDSLVLNNGFTHRSVPTTSTGVVSEBPTLNT 193
DB 279 GDRBOLYLIELSOLTHSITELEGPYTLDRDSLVLNNGFTHRSVPTTSTGVVSEBPTLNT 338
QY 194 INNLRYADMGOGSLKFNITDVMVKHLSPFORSLGARVYGCRIYALRSYNGAETR 253
DB 339 INNLRYADMGOGSLKFNITDVMVKHLSPFORSLGARVYGCRIYALRSYNGAETR 398
QY 254 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGIRLGPYSIDKDSLVLNNGNEBGPDEPPT 313
DB 399 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGIRLGPYSIDKDSLVLNNGNEBGPDEPPT 458
QY 314 TPKPATTFLPPLSBATTAMGYHLKTLTNTISNLQYSPMGKGSATFNSTEGVLOHLR 373

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Db      459 TPKATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSGVLQHLR 518
      374 PLFQKSMGPFYLGCOLISLRPEKGAATGVDITCTTHPDVPGGLDIQQLYWELSQLT 433
      519 PLFQKSMGPFYLGCOLISLRPEKGAATGVDITCTTHPDVPGGLDIQQLYWELSQLT 578
Qy      434 GVTQLGFYVLDRLSLFNGVAPQNLSTIRGEYQINPHVNMNLSNPDPTSSSEYITLLDIO 493
      579 GVTQLGFYVLDRLSLFNGVAPQNLSTIRGEYQINPHVNMNLSNPDPTSSSEYITLLDIO 638
Qy      494 DKVTLLYKGSQLDHTEFPCLVNTLTMDSVLTVALFPSSNLDPSLVEQVFLDKTLNASFH 553
      639 DKVTLLYKGSQLDHTEFPCLVNTLTMDSVLTVALFPSSNLDPSLVEQVFLDKTLNASFH 698
Db      554 WLGSYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDAQPGTTNYQNRK 613
      699 WLGSYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDAQPGTTNYQNRK 758
Qy      614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLGNPSPLARRVDAIYEEF 673
      759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLGNPSPLARRVDAIYEEF 818
Db      674 LRMTNGTQLQNFLLDRSSVLDGYSPNREPLTGN 710
      819 LRMTNGTQLQNFLLDRSSVLDGYSPNREPLTGN 855

```

RESULT 13

ABP30896 standard; protein; 914 AA.

ID ABP30896

AC ABP30896;

DT 02-JUL-2002 (first entry)

XX 0772P protein.

KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.

OS Homo sapiens.

PN MO200206317-A2.

PD 24-JAN-2002.

PF 17-JUL-2001; 2001WO-US022635.

PR 17-JUL-2000; 2000US-00617747.

PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.

PR 04-APR-2001; 2001US-00827271.

PR 18-JUN-2001; 2001US-00884441.

PA (CORI-) CORIXA CORP.

PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;

PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;

PT WPI; 2002-164781/21.

DR N-PSDB; ABN72895.

XX

XX

XX

XX

```

CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX      SQ      Sequence 914 AA;
      Query Match      92.9%; Score 3663; DB 5; Length 914;
      Best Local Similarity 99.9%; Pred. No. 2,7e-315;
      Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      14 FTHRSSVSTSTPTGPTFVYIGAKTPASIFGSAASHLLILFTLNFTITNLRYEENMPG 73
      159 FTHRSSVSTSTPTGPTFVYIGAKTPASIFGSAASHLLILFTLNFTITNLRYEENMPG 216
Db      74 SRKFNTERLQGLNPLRFKNTSVGPYSGCRLLLRPEKGAATGVDALCTHRPDDTGP 133
      219 SRKFNTERLQGLNPLRFKNTSVGPYSGCRLLLRPEKGAATGVDALCTHRPDDTGP 278
Qy      134 GLDREQLYLELSQLTSLITELGPTLDRDSLAVNGFTHRSSVPTSTGVSEEFITNFT 193
      279 GLDREQLYLELSQLTSLITELGPTLDRDSLAVNGFTHRSSVPTSTGVSEEFITNFT 338
Db      194 INNLRYADWGQPGSLKENITDVMKLLSPLFQSSLGARYTCRYIALRSYNGAETR 253
      339 INNLRYADWGQPGSLKENITDVMKLLSPLFQSSLGARYTCRYIALRSYNGAETR 398
Qy      254 VDLICTYLOPLSGPGPIKQVFEHLSQTHGTRGLGPISLDKSLYNGNBPDPPT 313
      399 VDLICTYLOPLSGPGPIKQVFEHLSQTHGTRGLGPISLDKSLYNGNBPDPPT 458
Db      314 TPKATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSGVLQHLR 373
      459 TPKATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSGVLQHLR 518
Qy      374 PLFQKSMGPFYLGCOLISLRPEKGAATGVDITCTTHPDVPGGLDIQQLYWELSQLT 433
      519 PLFQKSMGPFYLGCOLISLRPEKGAATGVDITCTTHPDVPGGLDIQQLYWELSQLT 578
Db      434 GVTQLGFYVLDRLSLFNGVAPQNLSTIRGEYQINPHVNMNLSNPDPTSSSEYITLLDIO 493
      579 GVTQLGFYVLDRLSLFNGVAPQNLSTIRGEYQINPHVNMNLSNPDPTSSSEYITLLDIO 638
Qy      494 DKVTLLYKGSQLDHTEFPCLVNTLTMDSVLTVALFPSSNLDPSLVEQVFLDKTLNASFH 553
      639 DKVTLLYKGSQLDHTEFPCLVNTLTMDSVLTVALFPSSNLDPSLVEQVFLDKTLNASFH 698
Db      554 WLGSYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDAQPGTTNYQNRK 613
      699 WLGSYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDAQPGTTNYQNRK 758
Qy      614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLGNPSPLARRVDAIYEEF 673
      759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLGNPSPLARRVDAIYEEF 818
Db      674 LRMTNGTQLQNFLLDRSSVLDGYSPNREPLTGN 710
      819 LRMTNGTQLQNFLLDRSSVLDGYSPNREPLTGN 855

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RESULT 14

ADU01425 standard; protein; 914 AA.

ID ADU01425

AC ADU01425;

DT 30-DEC-2004 (first entry)

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XX

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CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX      SQ      Sequence 914 AA;
      Query Match      92.9%; Score 3663; DB 5; Length 914;
      Best Local Similarity 99.9%; Pred. No. 2,7e-315;
      Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      14 FTHRSSVSTSTPTGPTFVYIGAKTPASIFGSAASHLLILFTLNFTITNLRYEENMPG 73
      159 FTHRSSVSTSTPTGPTFVYIGAKTPASIFGSAASHLLILFTLNFTITNLRYEENMPG 216
Db      74 SRKFNTERLQGLNPLRFKNTSVGPYSGCRLLLRPEKGAATGVDALCTHRPDDTGP 133
      219 SRKFNTERLQGLNPLRFKNTSVGPYSGCRLLLRPEKGAATGVDALCTHRPDDTGP 278
Qy      134 GLDREQLYLELSQLTSLITELGPTLDRDSLAVNGFTHRSSVPTSTGVSEEFITNFT 193
      279 GLDREQLYLELSQLTSLITELGPTLDRDSLAVNGFTHRSSVPTSTGVSEEFITNFT 338
Db      194 INNLRYADWGQPGSLKENITDVMKLLSPLFQSSLGARYTCRYIALRSYNGAETR 253
      339 INNLRYADWGQPGSLKENITDVMKLLSPLFQSSLGARYTCRYIALRSYNGAETR 398
Qy      254 VDLICTYLOPLSGPGPIKQVFEHLSQTHGTRGLGPISLDKSLYNGNBPDPPT 313
      399 VDLICTYLOPLSGPGPIKQVFEHLSQTHGTRGLGPISLDKSLYNGNBPDPPT 458
Db      314 TPKATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSGVLQHLR 373
      459 TPKATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSGVLQHLR 518
Qy      374 PLFQKSMGPFYLGCOLISLRPEKGAATGVDITCTTHPDVPGGLDIQQLYWELSQLT 433
      519 PLFQKSMGPFYLGCOLISLRPEKGAATGVDITCTTHPDVPGGLDIQQLYWELSQLT 578
Db      434 GVTQLGFYVLDRLSLFNGVAPQNLSTIRGEYQINPHVNMNLSNPDPTSSSEYITLLDIO 493
      579 GVTQLGFYVLDRLSLFNGVAPQNLSTIRGEYQINPHVNMNLSNPDPTSSSEYITLLDIO 638
Qy      494 DKVTLLYKGSQLDHTEFPCLVNTLTMDSVLTVALFPSSNLDPSLVEQVFLDKTLNASFH 553
      639 DKVTLLYKGSQLDHTEFPCLVNTLTMDSVLTVALFPSSNLDPSLVEQVFLDKTLNASFH 698
Db      554 WLGSYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDAQPGTTNYQNRK 613
      699 WLGSYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDAQPGTTNYQNRK 758
Qy      614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLGNPSPLARRVDAIYEEF 673
      759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLGNPSPLARRVDAIYEEF 818
Db      674 LRMTNGTQLQNFLLDRSSVLDGYSPNREPLTGN 710
      819 LRMTNGTQLQNFLLDRSSVLDGYSPNREPLTGN 855

```

RESULT 14

ADU01425 standard; protein; 914 AA.

ID ADU01425

AC ADU01425;

DT 30-DEC-2004 (first entry)

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PN US2002081609-A1.
 XX 27-JUN-2002.
 PD
 XX 20-JUL-2001; 2001US-00910689.
 XX
 PR 30-NOV-1999; 99US-00451651.
 PR 22-FEB-2000; 2000US-00510662.
 PR 10-MAR-2000; 2000US-00523586.
 PR 07-APR-2000; 2000US-00545068.
 PR 15-MAY-2000; 2000US-00571025.
 PR 06-FEB-2001; 2001US-00778320.
 XX
 PA (DILL/) DILLON D. C.
 PA (DAYC/) DAY C. H.
 PA (JIAN/) JIANG Y.
 PA (HOUG/) HOUGHTON R. L.
 PA (MITC/) MITCHAM J. L.
 PA (WANG/) WANG T.
 PA (MCMB/) MCNEILL P. D.
 PA (HARL/) HARLOCKER S. L.
 PI
 PI Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T,
 PI McNeill PD, Harlocker SL,
 DR WPI, 2002-657500/70.
 DR N-PSDB; ADU01424.
 PT Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 XX
 PS Claim 2; SEQ ID NO 206; 159pp; English.
 XX
 CC The invention describes an isolated breast cancer polynucleotide (I)
 CC comprising a sequence (S1) selected from the 249 nucleotide sequences
 CC fully defined in the specification, complements of S1, a sequence
 CC comprising at least 20 contiguous residues of S1, a sequence that
 CC hybridize to S1, under moderately stringent conditions, a sequence having
 CC at least 75%, preferably 90% identity to S1, or degenerate variants of
 CC S1. Also described are: an isolated polypeptide (II) encoded by (I), or
 CC sequences having at least 70%, preferably 90% identity to (I); an
 CC expression vector (III); a host cell (IV) transformed or transfected with
 CC (III); an isolated antibody (Ab) that specifically binds to (II);
 CC detecting (M1) the presence of cancer in a patient; a fusion protein (V)
 CC comprising (II); an oligonucleotide (VI) that hybridizes to S1;
 CC stimulating and/or expanding (M2) T cells specific for a tumour protein;
 CC a composition (C) comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC (I), (II), Ab, (V), (VII) and antigen presenting cells that express (II);
 CC and inhibiting (M3) the development of a cancer in a patient. (C) is
 CC useful for stimulating immune response in a patient, and for treating
 CC cancer in a patient. (VI) is useful for determining the presence of
 CC cancer in a patient, by obtaining a biological sample from the patient,
 CC contacting the biological sample with a monoclonal antibody that bind to
 CC O6B, isolating cells that bind to the antibody that binds to O6B,
 CC isolating polynucleotides from the isolated cells, and contacting the
 CC polynucleotides with (VI), detecting an amount of polynucleotides that
 CC hybridize to the oligonucleotide, and comparing the amount of
 CC polynucleotides that hybridize to the oligonucleotide to a predetermined
 CC cut-off value, and thus determining the presence of cancer in the
 CC patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
 CC vaccines. (I) is useful in the design and preparation of ribozyme
 CC molecules for inhibiting expression of the tumour polypeptides and
 CC proteins in tumour cells. (I) is useful as marker to indicate the
 CC presence or absence of a cancer such as breast cancer. (C) is useful for
 CC inhibiting the development of breast cancer in a patient, and for
 CC removing tumour cells from a biological sample. Ab binding agent for
 CC (I) is useful for detecting the presence of cancer in a patient. This
 CC sequence represents a breast cancer associated protein.
 XX
 SEQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 5; Length 914;
 Best Local Similarity 99.9%; Pred. No. 2.7e-315;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 219 SRKFNTTFRVIGQLRPLFKNTSVGLYSGCRLTLRPEKDEATGVDAICTHRDPPTCP 278
 QY 134 GLDRPOLVLELSQTLHSITELGPTLDRDSLVLVNGFTHRSVPTTSTGVSEEPPLNFT 193
 DB 279 GLDRPOLVLELSQTLHSITELGPTLDRDSLVLVNGFTHRSVPTTSTGVSEEPPLNFT 338
 QY 194 INNLRVYMDMGQPGSLKRNITDNNVKKHLLSPFGSSSLGARVTGCRVIALRNVKGAETR 253
 DB 339 INNLRVYMDMGQPGSLKRNITDNNVKKHLLSPFGSSSLGARVTGCRVIALRNVKGAETR 398
 QY 254 VDLCTYLOPLSGPGLPIKQVFEHSQOHTGTRLGPSLDDSLYLNGVNEPDPDEPPT 313
 DB 399 VDLCTYLOPLSGPGLPIKQVFEHSQOHTGTRLGPSLDDSLYLNGVNEPDPDEPPT 458
 QY 314 TPKPATTFPLPSEATTAMGYHLKTLINFTISNLQYSPDMGKSGATFNSTGVLQHLIR 373
 DB 459 TPKPATTFPLPSEATTAMGYHLKTLINFTISNLQYSPDMGKSGATFNSTGVLQHLIR 518
 QY 374 PLFOKSSMGPPFLGCOLISLRPEKGAATGVTTCTTHPDPVPGDLIOQLVWEISQLTH 433
 DB 519 PLFOKSSMGPPFLGCOLISLRPEKGAATGVTTCTTHPDPVPGDLIOQLVWEISQLTH 578
 QY 434 GYTOLGFFVLDLDRDSLFINGYAPONLSIRGEYOINFIHVMNLSNPPTSSEYITLLRDIO 493
 DB 579 GYTOLGFFVLDLDRDSLFINGYAPONLSIRGEYOINFIHVMNLSNPPTSSEYITLLRDIO 638
 QY 494 DKVTLLYKSSQLHDPFRFLVNTLMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASH 553
 DB 639 DKVTLLYKSSQLHDPFRFLVNTLMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASH 698
 QY 554 WIGSTYQVLVDIHVTEMESSVYOPTSSSTQHFILANTTNLPISQKAPGTTNYQRNR 613
 DB 699 WIGSTYQVLVDIHVTEMESSVYOPTSSSTQHFILANTTNLPISQKAPGTTNYQRNR 758
 QY 614 NIEDALNOLFRNSSISYSDQVSTFRSVPNRHGTVDSLCNFSPILARVDRAIYEEF 673
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 QY 674 LRWTRNGTQLQNTFLDRSSVLVDGYSPNNEPLTGN 710
 DB 819 LRWTRNGTQLQNTFLDRSSVLVDGYSPNNEPLTGN 855
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 ADZ41689
 ID ADZ41689 standard; protein; 914 AA.
 XX
 AC ADZ41689;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Human breast cancer associated protein SEQ ID NO 206.
 XX
 KM cytoabatic; gene therapy; vaccine; diagnosis; pharmaceutical; cancer;
 XX neoplasm; breast tumor; endocrine disease; gynecology and obstetrics.
 XX
 OS Homo sapiens.
 XX
 PN W0200262203-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 04-FEB-2002; 2002MO-US003332.

XX 06-FEB-2001; 2001US-00778320.
 PR 20-JUL-2001; 2001US-00910689.
 PR 30-NOV-2001; 2001US-00010742.
 XX
 PA (CORI-) CORIXA CORP.
 PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;
 PI Menelli PD, Harlocker SL, Bennington AA, Zehentner B, Fanger GR;
 PI Reiter MW;
 XX
 DR MPI; 2002-657500/70.
 DR N-PSDB; ADZ41688.
 XX
 PT Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 XX
 PS Claim 2; SEQ ID NO 206, 237pp; English.
 XX
 CC The invention describes an isolated breast cancer polynucleotide (I)
 CC comprising a sequence (S1) selected from the 249 nucleotide sequences
 CC fully defined in the specification, complements of S1, a sequence
 CC comprising at least 20 contiguous residues of S1, a sequence that
 CC hybridize to S1, under moderately stringent conditions, a sequence having
 CC at least 75%, preferably 90% identity to S1, or degenerate variants of
 CC S1. Also described are: an isolated polypeptide (II) comprising a
 CC sequence (S2) selected from any one of the 11 sequences mentioned in the
 CC specification, sequences encoded by (I), or sequences having at least
 CC 70%, preferably 90% identity to (I); an expression vector (III)
 CC comprising (I), operably linked to an expression control sequence; a host
 CC cell (IV) transformed or transfected with (III); an isolated antibody
 CC (Ab) or its antigen-binding fragment, that specifically binds to (II);
 CC detecting (M1) the presence of cancer in a patient; a fusion protein (V)
 CC comprising (II); an oligonucleotide (VI) that hybridizes to S1;
 CC stimulating and/or expanding (M2) T cells specific for a tumor protein;
 CC an isolated T cell population (VII), comprising T cells prepared by (M2);
 CC a composition (C) comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC (I), (II), Ab, (V), (VII) and antigen presenting cells that express (II);
 CC a diagnostic kit (VIII) comprising (VI), or Ab and a detection reagent
 CC comprising a reporter group; and inhibiting (M3) the development of a
 CC cancer in a patient, by incubating CD4+ and/or CD8+ T cells isolated from
 CC a patient with (I), (II) or antigen presenting cells that express (II),
 CC so that T cell proliferate, administering the proliferated T cells to the
 CC patient, and therefore inhibiting the development of a cancer in the
 CC patient. The following are disclosed: monitoring the progression of
 CC cancer; fragments of (II); (xenogeneic) variants of (I); polynucleotide
 CC compositions comprising antisense oligonucleotide; and kit for use in
 CC diagnostic methods. (C) is useful for stimulating immune response in a
 CC patient, and for treating cancer in a patient. (VI) is useful for
 CC determining the presence of cancer in a patient. (I) and (II) are useful
 CC in pharmaceutical compositions, e.g., vaccines. (I) is useful in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC the tumor polypeptides and proteins in tumor cells. (I) is useful as
 CC marker to indicate the presence or absence of a cancer such as breast
 CC cancer. (C) is useful for inhibiting the development of breast cancer in
 CC a patient, and for removing tumor cells from a biological sample. Ab
 CC (binding agent for (I)) is useful for detecting the presence of cancer in
 CC a patient. This is the amino acid sequence of a breast cancer associated
 CC protein. Note: This sequence has been extracted from the sequence listing
 CC of a corrected version of the specification published on the 3rd of March
 CC 2005.
 XX
 SQ Sequence 914 AA:

Query Match 92.9%; Score 3663; DB 5; Length 914;
 Best Local Similarity 99.9%; Pred. No. 2.7e-315;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTGPTVYVYGASKTPASIRGSAASHLILFTLNFTITNLRYEENMMPG 73
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 DB 159 FTHRSSVSTSTGPTVYVYGASKTPASIRGSAASHLILFTLNFTITNLRYEENMMPG 218

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 DB 219 SRKENTTERVLOGLRPLFRNTSVGLYSGCRLTLRPEKDGATGVDAICTHRPDPGP 278
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 QY 134 GLDREQLYLELSQTHSITELGPTLDRSLVYNGFTHRSSVPTSTGVSEEPFTLNFT 193
 |||||||
 DB 279 GLDREQLYLELSQTHSITELGPTLDRSLVYNGFTHRSSVPTSTGVSEEPFTLNFT 338
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 QY 254 VDLCTTYLOPLSGRPIKQVFFHELSQOHTGTRGLPGLYDKDSLVLNGNEGPDEPPT 313
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 QY 314 TPKPATTFPLPSEATAMGYHLKTLTLNFTSNLQSPDMKGSATFNSBEGVLOHLR 373
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 DB 459 TPKPATTFPLPSEATAMGYHLKTLTLNFTSNLQSPDMKGSATFNSBEGVLOHLR 518
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 QY 434 GTYQLGFYVLDRLSLFINGYAPONLSIRGEYQINFIYVMNLSNPPTSSEYITLLRDIO 493
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 DB 579 GTYQLGFYVLDRLSLFINGYAPONLSIRGEYQINFIYVMNLSNPPTSSEYITLLRDIO 638
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 QY 494 DKVTLLYKSSQLHDPFRFLVNLTMDSVLVYKALFSSNLDPDLVEQVFLDTLNASFH 553
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 DB 639 DKVTLLYKSSQLHDPFRFLVNLTMDSVLVYKALFSSNLDPDLVEQVFLDTLNASFH 698
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 QY 554 WLGSTYQLVDIHVTMESSVYOPTSSSTOHFYLNFTITNLPSQDKAOPGTNYQRNKR 613
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 DB 699 WLGSTYQLVDIHVTMESSVYOPTSSSTOHFYLNFTITNLPSQDKAOPGTNYQRNKR 758
 |||||||
 QY 614 NIEDALNQLFRNSSISYSDCOVSTFRSVPNRHHGVDSLNFSPILARRVDRVAIYEER 673
 |||||||
 DB 759 NIEDALNQLFRNSSISYSDCOVSTFRSVPNRHHGVDSLNFSPILARRVDRVAIYEER 818
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 QY 674 LMRTRNGTOLNFTLDRSSVLVDGYSPPNRNEPLTGN 710
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 DB 819 LMRTRNGTOLNFTLDRSSVLVDGYPNRNEPLTGN 855
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 Job time : 208 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 14, 2006, 04:05:25 : Search time 185 Seconds

(without alignments)
1872.890 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945
Sequence: 1 AAQPARRRARTKXLFTHRSSV.....QKLISEEDLNMHTGHHHHH 748

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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6: /EMC_Ceitera_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	748	US-10-687-035-1	Sequence 1, Appl1
2	3904.5	99.0	809	US-10-687-035-2	Sequence 2, Appl1
3	3665	92.9	6995	US-10-983-340-4	Sequence 4, Appl1
4	3663	92.9	833	US-09-884-441-389	Sequence 389, App
5	3663	92.9	833	US-09-907-969-389	Sequence 389, App
6	3663	92.9	833	US-09-827-271-389	Sequence 389, App
7	3663	92.9	833	US-10-198-053-389	Sequence 389, App
8	3663	92.9	833	US-10-860-790-389	Sequence 389, App
9	3663	92.9	914	US-09-778-320-206	Sequence 206, App
10	3663	92.9	914	US-09-910-689-206	Sequence 206, App
11	3663	92.9	914	US-09-884-441-312	Sequence 312, App
12	3663	92.9	914	US-09-884-441-478	Sequence 478, App
13	3663	92.9	914	US-09-907-969-312	Sequence 312, App
14	3663	92.9	914	US-09-907-969-478	Sequence 478, App
15	3663	92.9	914	US-09-827-271-312	Sequence 312, App
16	3663	92.9	914	US-10-010-742-206	Sequence 206, App
17	3663	92.9	914	US-10-198-053-312	Sequence 312, App
18	3663	92.9	914	US-10-198-053-478	Sequence 478, App
19	3663	92.9	914	US-10-714-389-206	Sequence 206, App
20	3663	92.9	914	US-10-717-296-206	Sequence 206, App
21	3663	92.9	914	US-10-860-790-312	Sequence 312, App
22	3663	92.9	914	US-10-860-790-478	Sequence 478, App
23	3663	92.9	1889	US-10-142-515-5	Sequence 5, Appl1
24	3658	92.7	1890	US-10-097-340-217	Sequence 217, App
25	3658	92.7	1890	US-10-245-871-314	Sequence 314, App
26	3658	92.7	1890	US-10-253-286-314	Sequence 314, App
27	3658	92.7	1890	US-11-050-926-217	Sequence 217, App

28	3658	92.7	1890	6	US-11-033-039-314	Sequence 314, App
29	3651	92.5	3451	3	US-09-907-969-595	Sequence 595, App
30	3651	92.5	3451	4	US-10-198-053-595	Sequence 595, App
31	3651	92.5	3451	5	US-10-860-790-595	Sequence 595, App
32	3649	92.5	1148	3	US-09-965-738-48	Sequence 48, Appl1
33	3649	92.5	2248	3	US-09-965-738-50	Sequence 50, Appl1
34	3649	92.5	11721	3	US-09-965-738-162	Sequence 162, App
35	3649	92.5	22152	4	US-10-715-366-5	Sequence 5, Appl1
36	3642	92.3	1148	3	US-09-884-441-458	Sequence 458, App
37	3642	92.3	1148	3	US-09-884-441-479	Sequence 479, App
38	3642	92.3	1148	3	US-09-907-969-458	Sequence 458, App
39	3642	92.3	1148	3	US-09-907-969-479	Sequence 479, App
40	3642	92.3	1148	3	US-09-827-271-458	Sequence 458, App
41	3642	92.3	1148	4	US-10-097-340-216	Sequence 216, App
42	3642	92.3	1148	4	US-10-198-053-458	Sequence 458, App
43	3642	92.3	1148	4	US-10-198-053-479	Sequence 479, App
44	3642	92.3	1148	4	US-10-257-021-56	Sequence 56, Appl1
45	3642	92.3	1148	4	US-10-383-368-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-10-687-035-1
; Sequence 1, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; FILE REFERENCES: CA 125/0772P AND METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/687,035
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat
US-10-687-035-1
Query Match 100.0%; Score 3945; DB 5; Length 748;
Best Local Similarity 100.0%; Pred. No. 3.4e-312;
Matches 748; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AAQPARRRARTKXLFTHRSSVSTSTPGTPVYVYGASGTPSIFGSAASHLLFLFTNFT 60
1 ITMLRYEENMPPGSRKFNTERVLOGLRLPFGNTSGVPLYSGRCLTLRLPEKDEATGV 120
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1 ITMLRYEENMPPGSRKFNTERVLOGLRLPFGNTSGVPLYSGRCLTLRLPEKDEATGV 120
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QY 301 NCYNERGDEPPTTPKPAATFLPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSAT 360
DB 301 NCYNERGDEPPTTPKPAATFLPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSAT 360
QY 361 FNSTGVLQHLRLPFLFKSKMGPFLYGCOLISLRPEKDAATGVDTTCYHDPVPGAD 420
DB 361 FNSTGVLQHLRLPFLFKSKMGPFLYGCOLISLRPEKDAATGVDTTCYHDPVPGAD 420
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RESULT 2
US-10-687-035-2
Sequence 2, Application US/10687035
Publication No. US20050064518A1
GENERAL INFORMATION:
APPLICANT: Albione, Earl F.
APPLICANT: Solitis, Daniel A.
TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
FILE REFERENCE: 6750-214-999
CURRENT APPLICATION NUMBER: US/10/687,035
PRIOR FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/485,986
PRIOR FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: 60/418,828
PRIOR FILING DATE: 2003-10-12
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 809
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CA 125/0772P 3-repeat TM
US-10-687-035-2

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Best Local Similarity 92.5%; Pred. No. 7.7e-309;
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DB 721 SLEGPREFOKLISEEDLNMTGHHHHH 748
QY 781 SLEGPREFOKLISEEDLNMTGHHHHH 809
DB 781 SLEGPREFOKLISEEDLNMTGHHHHH 809

RESULT 3
US-10-983-340-4
Sequence 4, Application US/10983340
Publication No. US20050238649A1
GENERAL INFORMATION:
APPLICANT: Doronina, Svetlana O.
APPLICANT: Toki, Brian E.
APPLICANT: Senter, Peter D.
APPLICANT: Ebens, Allen J.
APPLICANT: Polakis, Paul
APPLICANT: Sliwowski, Mark X.
APPLICANT: Spencer, Susan D.
APPLICANT: Kline, Toni Beth
TITLE OF INVENTION: MONOMETHYLVALINE COMPOUNDS CAPABLE OF CONJUGATION TO LIGANDS
FILE REFERENCE: 018691-001020US
CURRENT APPLICATION NUMBER: US/10/983,340
PRIOR FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US 60/598,899
PRIOR FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: US 60/557,116
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 60/518,534
PRIOR FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 4
LENGTH: 6995

TYPE: PRT
ORGANISM: Homo sapien
US-10-983-340-4

Query Match 92.9%; Score 3665; DB 5; Length 6995;
Best Local Similarity 99.9%; Pred. No. 7.5e-288;
Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 14 FTHRSSVSTSTGCTPTVYLGASKTSPASIFGSPAASHLLILFTLNFTITNLRYENMMPG 73
DB 6240 FTHRSSVSTSTGCTPTVYLGASKTSPASIFGSPAASHLLILFTLNFTITNLRYENMMPG 6299
QY 74 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 6300 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 6359
QY 134 GLDREQLYELSQLTHSITELGPTLDRDSL YVNGFTHRSSVPTSTGVSEBPTLNFT 193
DB 6360 GLDREQLYELSQLTHSITELGPTLDRDSL YVNGFTHRSSVPTSTGVSEBPTLNFT 6419
QY 194 INNLRYADMGQPSGLKFNITDVMKHLSPFORSSLGARYTCRYIALRSVNGAETR 253
DB 6420 INNLRYADMGQPSGLKFNITDVMKHLSPFORSSLGARYTCRYIALRSVNGAETR 6479
QY 254 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGTRIGPYSLDKDSL YVNGVNEBGPDPPT 313
DB 6480 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGTRIGPYSLDKDSL YVNGVNEBGPDPPT 6539
QY 314 TPXPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSTEGVLQHLR 373
DB 6540 TPXPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSTEGVLQHLR 6599
QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIOQLYELSQLTH 433
DB 6600 PLFOKSMGPFYLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIOQLYELSQLTH 6659
QY 434 GVTQLGYYVLDRLSLFNGYAPONLSIRGEYQINPHVNMNLSNPDPSTSEYITLLDIO 493
DB 6660 GVTQLGYYVLDRLSLFNGYAPONLSIRGEYQINPHVNMNLSNPDPSTSEYITLLDIO 6719
QY 494 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLTVAKALFSSNLDPSELVEQVFLDKTLNASFH 553
DB 6720 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLTVAKALFSSNLDPSELVEQVFLDKTLNASFH 6779
QY 554 WLGSTYQVLDIHVTEMESYVQPTSSSTQHFYLNFTITNL PYSQDAQPGTNYQNKR 613
DB 6780 WLGSTYQVLDIHVTEMESYVQPTSSSTQHFYLNFTITNL PYSQDAQPGTNYQNKR 6839
QY 614 NIDDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDAIYEEF 673
DB 6840 NIDDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDAIYEEF 6899
QY 674 LRMTNRGTOLQNFLLDRSSVLYVDGYSNNRNEPLTGN 710
DB 6900 LRMTNRGTOLQNFLLDRSSVLYVDGYSNNRNEPLTGN 6936
```

RESULT 4
US-09-884-441-389
Sequence 389, Application US/09884441
Patent No. US20020119158A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884.441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 389
LENGTH: 833

TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-441-389

Query Match 92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 4e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 14 FTHRSSVSTSTGCTPTVYLGASKTSPASIFGSPAASHLLILFTLNFTITNLRYENMMPG 73
DB 78 FTHRSSVSTSTGCTPTVYLGASKTSPASIFGSPAASHLLILFTLNFTITNLRYENMMPG 137
QY 74 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 138 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 197
QY 134 GLDREQLYELSQLTHSITELGPTLDRDSL YVNGFTHRSSVPTSTGVSEBPTLNFT 193
DB 198 GLDREQLYELSQLTHSITELGPTLDRDSL YVNGFTHRSSVPTSTGVSEBPTLNFT 257
QY 194 INNLRYADMGQPSGLKFNITDVMKHLSPFORSSLGARYTCRYIALRSVNGAETR 253
DB 258 INNLRYADMGQPSGLKFNITDVMKHLSPFORSSLGARYTCRYIALRSVNGAETR 317
QY 254 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGTRIGPYSLDKDSL YVNGVNEBGPDPPT 313
DB 318 VDLCTYLOPLSGPGLPIKOVFHELSQOHTGTRIGPYSLDKDSL YVNGVNEBGPDPPT 377
QY 314 TPXPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSTEGVLQHLR 373
DB 378 TPXPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPMGKGSATFNSTEGVLQHLR 437
QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIOQLYELSQLTH 433
DB 438 PLFOKSMGPFYLGCOLISLRPEKGAATGVTTCYHPDPVPGGLDIOQLYELSQLTH 497
QY 434 GVTQLGYYVLDRLSLFNGYAPONLSIRGEYQINPHVNMNLSNPDPSTSEYITLLDIO 493
DB 498 GVTQLGYYVLDRLSLFNGYAPONLSIRGEYQINPHVNMNLSNPDPSTSEYITLLDIO 557
QY 494 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLTVAKALFSSNLDPSELVEQVFLDKTLNASFH 553
DB 558 DKYTTLYKGSQLDHTRFCLVTNLTMDSVLTVAKALFSSNLDPSELVEQVFLDKTLNASFH 617
QY 554 WLGSTYQVLDIHVTEMESYVQPTSSSTQHFYLNFTITNL PYSQDAQPGTNYQNKR 613
DB 618 WLGSTYQVLDIHVTEMESYVQPTSSSTQHFYLNFTITNL PYSQDAQPGTNYQNKR 677
QY 614 NIDDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDAIYEEF 673
DB 678 NIDDALNQLFRNSIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDAIYEEF 737
QY 674 LRMTNRGTOLQNFLLDRSSVLYVDGYSNNRNEPLTGN 710
DB 738 LRMTNRGTOLQNFLLDRSSVLYVDGYSNNRNEPLTGN 774
```

RESULT 5
US-09-907-969-389
Sequence 389, Application US/09907969
Publication No. US20030091580A1
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Piling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Ronger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Hill, Paul
APPLICANT: Albane, Earl

```
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C8
/ CURRENT APPLICATION NUMBER: US/09/907,969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 389
/ LENGTH: 833
/ TYPE: PRN
/ ORGANISM: Homo sapiens
US-09-907-969-389
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Query Match      92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 4e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTTINLRYEENMWDG 73
DB 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTTINLRYEENMWDG 137

QY 74 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133
DB 138 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197

QY 134 GLDREOLYLELSOLTHSITELGPTLDRDSLVLVNGFTHRSSVPTSTGVVSEEPFLNT 193
DB 198 GLDREOLYLELSOLTHSITELGPTLDRDSLVLVNGFTHRSSVPTSTGVVSEEPFLNT 257

QY 194 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSLGARYGCRVIALRSYONAEFR 253
DB 258 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSLGARYGCRVIALRSYONAEFR 317

QY 254 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGTRGLRPLSLDKDSLVLNGNEBGPDEPPT 313
DB 318 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGTRGLRPLSLDKDSLVLNGNEBGPDEPPT 377

QY 314 TPKPATTFPLPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSGATFNSTBGVLOHLR 373
DB 378 TPKPATTFPLPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSGATFNSTBGVLOHLR 437

QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIQOLYWELSOLTH 433
DB 438 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIQOLYWELSOLTH 497

QY 434 GTVQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVNMNLSNPDTSEYITLLRDIO 493
DB 498 GTVQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVNMNLSNPDTSEYITLLRDIO 557

QY 494 DKYTTLYKGSQQLHDTFRFCLVTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 558 DKYTTLYKGSQQLHDTFRFCLVTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNASFH 617

QY 554 WLGSSTYQVLDIHTEMSSVYOPTSSSTQHFYLNFTITNLPSYQDAQAGTTNYQNK 613
DB 618 WLGSSTYQVLDIHTEMSSVYOPTSSSTQHFYLNFTITNLPSYQDAQAGTTNYQNK 677

QY 614 NIDBALNQLFRNSISIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDVAIYEEF 673
DB 678 NIDBALNQLFRNSISIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDVAIYEEF 737

QY 674 LRMTNRGTOLONFTLDRSSVLYVGYSPNRNEPPLTGN 710
DB 738 LRMTNRGTOLONFTLDRSSVLYVGYSPNRNEPPLTGN 774
```

```
RESULT 6
US-09-827-271-389
/ Sequence 389, Application US/0987271
/ Publication No. US20030165504A1
/ GENERAL INFORMATION:
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
```

```
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C6
/ CURRENT APPLICATION NUMBER: US/09/827,271
/ CURRENT FILING DATE: 2001-04-04
/ NUMBER OF SEQ ID NOS: 461
/ SOFTWARE: FaastSeq for Windows Version 3.0
/ SEQ ID NO 389
/ LENGTH: 833
/ TYPE: PRN
/ ORGANISM: Homo sapiens
US-09-827-271-389
```

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Query Match      92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 4e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTTINLRYEENMWDG 73
DB 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTTINLRYEENMWDG 137

QY 74 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133
DB 138 SRKFNTERVLOGLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197

QY 134 GLDREOLYLELSOLTHSITELGPTLDRDSLVLVNGFTHRSSVPTSTGVVSEEPFLNT 193
DB 198 GLDREOLYLELSOLTHSITELGPTLDRDSLVLVNGFTHRSSVPTSTGVVSEEPFLNT 257

QY 194 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSLGARYGCRVIALRSYONAEFR 253
DB 258 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSLGARYGCRVIALRSYONAEFR 317

QY 254 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGTRGLRPLSLDKDSLVLNGNEBGPDEPPT 313
DB 318 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGTRGLRPLSLDKDSLVLNGNEBGPDEPPT 377

QY 314 TPKPATTFPLPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSGATFNSTBGVLOHLR 373
DB 378 TPKPATTFPLPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSGATFNSTBGVLOHLR 437

QY 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIQOLYWELSOLTH 433
DB 438 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTYHPDPVPGGLDIQOLYWELSOLTH 497

QY 434 GTVQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVNMNLSNPDTSEYITLLRDIO 493
DB 498 GTVQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVNMNLSNPDTSEYITLLRDIO 557

QY 494 DKYTTLYKGSQQLHDTFRFCLVTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 558 DKYTTLYKGSQQLHDTFRFCLVTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNASFH 617

QY 554 WLGSSTYQVLDIHTEMSSVYOPTSSSTQHFYLNFTITNLPSYQDAQAGTTNYQNK 613
DB 618 WLGSSTYQVLDIHTEMSSVYOPTSSSTQHFYLNFTITNLPSYQDAQAGTTNYQNK 677

QY 614 NIDBALNQLFRNSISIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDVAIYEEF 673
DB 678 NIDBALNQLFRNSISIKSYFSDCOVSTFRSVPNRHHTGVDSL CNFSPILARRVDVAIYEEF 737

QY 674 LRMTNRGTOLONFTLDRSSVLYVGYSPNRNEPPLTGN 710
DB 738 LRMTNRGTOLONFTLDRSSVLYVGYSPNRNEPPLTGN 774
```

```
RESULT 7
US-10-198-053-389
/ Sequence 389, Application US/10198053
/ Publication No. US20030124140A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chalcanya S.
/ APPLICANT: Retter, Marc W.
```

```

; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-389

```

```

Query Match          92.9%; Score 3663; DB 4; Length 833;
Best Local Similarity 99.9%; Pred. No. 4e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 14 FTHRSSVSTSTGPTPTVYIGASKTPASIFGPSASHLLILFTLNFTITNLRYEENMPG 73
DB 78 FTHRSSVSTSTGPTPTVYIGASKTPASIFGPSASHLLILFTLNFTITNLRYEENMPG 137
QY 74 SRKFNTERVLOGLRLPLFNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDTGP 133
DB 138 SRKFNTERVLOGLRLPLFNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDTGP 197
QY 134 GLDREOLYLELSQTLHSITELGPTLDRDSLRYNGFTHRSSVPTTSGVSEEPFTLNFT 193
DB 198 GLDREOLYLELSQTLHSITELGPTLDRDSLRYNGFTHRSSVPTTSGVSEEPFTLNFT 257
QY 194 INNLRYADMGGGSLKFNITDVMKHLSPLEFORSSLGARYTCRVALRSYKNGAETR 253
DB 258 INNLRYADMGGGSLKFNITDVMKHLSPLEFORSSLGARYTCRVALRSYKNGAETR 317
QY 254 VDLICTYLOPLSGRGLPIKQVFNHLSQOHTGIRLGRPLSDKSLYNGVNEPQDPBPPT 313
DB 318 VDLICTYLOPLSGRGLPIKQVFNHLSQOHTGIRLGRPLSDKSLYNGVNEPQDPBPPT 377
QY 314 TPXPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB 378 TPXPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 437
QY 374 PLFOKSMGPFYLGCOLISLRPEKDGATGVDITCTYHPDPVPGGLDIQOLYWELSQLTH 433
DB 438 PLFOKSMGPFYLGCOLISLRPEKDGATGVDITCTYHPDPVPGGLDIQOLYWELSQLTH 497
QY 434 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYQINFIHVMNLSNPDPTSEYITLLRDIO 493
DB 498 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYQINFIHVMNLSNPDPTSEYITLLRDIO 557
QY 494 DKYTTLYKGSQQLDTRFRCLVTNLTMDSVLYVYKALFSSNLDPDLVEOVFLDXTLNASFH 553
DB 558 DKYTTLYKGSQQLDTRFRCLVTNLTMDSVLYVYKALFSSNLDPDLVEOVFLDXTLNASFH 617
QY 554 WLGSTYQVLDIVHTEMESSYVOPTSSSTOHHFYLNFTITNLPSQDKAOGTTNYQRNKR 613
DB 618 WLGSTYQVLDIVHTEMESSYVOPTSSSTOHHFYLNFTITNLPSQDKAOGTTNYQRNKR 677
QY 614 NIEDALNOLFRRNSISYSPDCOVSTFRSVPNRHHGTGVDSLCNFSPLARVDRVAIYEER 673
DB 678 NIEDALNOLFRRNSISYSPDCOVSTFRSVPNRHHGTGVDSLCNFSPLARVDRVAIYEER 737
QY 674 LRMTNRGTOLQONFTLDRSSVLYVGYSPNREPLTGN 710
DB 738 LRMTNRGTOLQONFTLDRSSVLYVGYSPNREPLTGN 774

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RESULT 8
US-10-860-790-389
; Sequence 389, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Bangur, Chalcanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860.790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-389

```

```

Query Match          92.9%; Score 3663; DB 5; Length 833;
Best Local Similarity 99.9%; Pred. No. 4e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 14 FTHRSSVSTSTGPTPTVYIGASKTPASIFGPSASHLLILFTLNFTITNLRYEENMPG 73
DB 78 FTHRSSVSTSTGPTPTVYIGASKTPASIFGPSASHLLILFTLNFTITNLRYEENMPG 137
QY 74 SRKFNTERVLOGLRLPLFNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDTGP 133
DB 138 SRKFNTERVLOGLRLPLFNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDTGP 197
QY 134 GLDREOLYLELSQTLHSITELGPTLDRDSLRYNGFTHRSSVPTTSGVSEEPFTLNFT 193
DB 198 GLDREOLYLELSQTLHSITELGPTLDRDSLRYNGFTHRSSVPTTSGVSEEPFTLNFT 257
QY 194 INNLRYADMGGGSLKFNITDVMKHLSPLEFORSSLGARYTCRVALRSYKNGAETR 253
DB 258 INNLRYADMGGGSLKFNITDVMKHLSPLEFORSSLGARYTCRVALRSYKNGAETR 317
QY 254 VDLICTYLOPLSGRGLPIKQVFNHLSQOHTGIRLGRPLSDKSLYNGVNEPQDPBPPT 313
DB 318 VDLICTYLOPLSGRGLPIKQVFNHLSQOHTGIRLGRPLSDKSLYNGVNEPQDPBPPT 377
QY 314 TPXPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB 378 TPXPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 437
QY 374 PLFOKSMGPFYLGCOLISLRPEKDGATGVDITCTYHPDPVPGGLDIQOLYWELSQLTH 433
DB 438 PLFOKSMGPFYLGCOLISLRPEKDGATGVDITCTYHPDPVPGGLDIQOLYWELSQLTH 497
QY 434 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYQINFIHVMNLSNPDPTSEYITLLRDIO 493
DB 498 GVTOLGFYVLDRLSLFINGYAPONLSIRGEYQINFIHVMNLSNPDPTSEYITLLRDIO 557
QY 494 DKYTTLYKGSQQLDTRFRCLVTNLTMDSVLYVYKALFSSNLDPDLVEOVFLDXTLNASFH 553
DB 558 DKYTTLYKGSQQLDTRFRCLVTNLTMDSVLYVYKALFSSNLDPDLVEOVFLDXTLNASFH 617
QY 554 WLGSTYQVLDIVHTEMESSYVOPTSSSTOHHFYLNFTITNLPSQDKAOGTTNYQRNKR 613
DB 618 WLGSTYQVLDIVHTEMESSYVOPTSSSTOHHFYLNFTITNLPSQDKAOGTTNYQRNKR 677
QY 614 NIEDALNOLFRRNSISYSPDCOVSTFRSVPNRHHGTGVDSLCNFSPLARVDRVAIYEER 673
DB 678 NIEDALNOLFRRNSISYSPDCOVSTFRSVPNRHHGTGVDSLCNFSPLARVDRVAIYEER 737
QY 674 LRMTNRGTOLQONFTLDRSSVLYVGYSPNREPLTGN 710
DB 738 LRMTNRGTOLQONFTLDRSSVLYVGYSPNREPLTGN 774

```

```

RESULT 9
US-09-778-320-206
; Sequence 206, Application US/09778320

```

```

; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,330
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-778-320-206

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Query Match      92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4,6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

14 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTINLRYEENMMPG 73
159 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTINLRYEENMMPG 218
74 SRKFNTEBVLQGLRLPLFKNTSVGLYSGCRLTLRLPEKDEAGVDAICTHRPDPGP 133
219 SRKFNTEBVLQGLRLPLFKNTSVGLYSGCRLTLRLPEKDEAGVDAICTHRPDPGP 278
134 GDRBQLYELSQLTHSITELGPTLDRDSLVLNGFTHRSVPPTSTGVSEEPFLNPT 193
279 GDRBQLYELSQLTHSITELGPTLDRDSLVLNGFTHRSVPPTSTGVSEEPFLNPT 338
194 INNLRYAMMGQPGSLKFNITDVMKHLSPFORSSLAGRYTGCRVIALRSYKNGAEFR 253
339 INNLRYAMMGQPGSLKFNITDVMKHLSPFORSSLAGRYTGCRVIALRSYKNGAEFR 398
254 VDLCTYLOPLSGPGLPIKQVFHLSQTHGIRLGRYSIDKDSLVLNGYNEBPDPEPT 313
399 VDLCTYLOPLSGPGLPIKQVFHLSQTHGIRLGRYSIDKDSLVLNGYNEBPDPEPT 458
314 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSAATFNSTEGVLOHLR 373
459 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSAATFNSTEGVLOHLR 518
374 PLFOKSMGPFYLGCOLISLRPEKGAAGVDTTCYHDPVPGGLDIQQLYELSQLTH 433
519 PLFOKSMGPFYLGCOLISLRPEKGAAGVDTTCYHDPVPGGLDIQQLYELSQLTH 578
434 GTVQLGFYVLDRLSLFINGYAPQNLIRGEYOINFIHVMNLSNPPTSSEYITLLRDIO 493
579 GTVQLGFYVLDRLSLFINGYAPQNLIRGEYOINFIHVMNLSNPPTSSEYITLLRDIO 638
494 DKVTLTKGSQLHDTFRFCVLTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNLSFH 553
639 DKVTLTKGSQLHDTFRFCVLTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNLSFH 698
554 WLGSTYQVLDIHTHEMESVYQPTSSSSTQHFIYLNFTITNLPSQDKAQPCTINYOQNR 613
699 WLGSTYQVLDIHTHEMESVYQPTSSSSTQHFIYLNFTITNLPSQDKAQPCTINYOQNR 758
614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSL CNFSPILARRVDAIYEEF 673
759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSL CNFSPILARRVDAIYEEF 818
674 LRMTRNGTOLNFTLDRSSVLVDGYSPNRNPLTNGS 710
819 LRMTRNGTOLNFTLDRSSVLVDGYSPNRNPLTNGS 855

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RESULT 10
US-09-910-689-206
; Sequence 206, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-910-689-206

```

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Query Match      92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4,6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

14 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTINLRYEENMMPG 73
159 FTHRSSVSTSTPGPTVYLGASKTPASIFGSAASHLLILFTLNFTINLRYEENMMPG 218
74 SRKFNTEBVLQGLRLPLFKNTSVGLYSGCRLTLRLPEKDEAGVDAICTHRPDPGP 133
219 SRKFNTEBVLQGLRLPLFKNTSVGLYSGCRLTLRLPEKDEAGVDAICTHRPDPGP 278
134 GDRBQLYELSQLTHSITELGPTLDRDSLVLNGFTHRSVPPTSTGVSEEPFLNPT 193
279 GDRBQLYELSQLTHSITELGPTLDRDSLVLNGFTHRSVPPTSTGVSEEPFLNPT 338
194 INNLRYAMMGQPGSLKFNITDVMKHLSPFORSSLAGRYTGCRVIALRSYKNGAEFR 253
339 INNLRYAMMGQPGSLKFNITDVMKHLSPFORSSLAGRYTGCRVIALRSYKNGAEFR 398
254 VDLCTYLOPLSGPGLPIKQVFHLSQTHGIRLGRYSIDKDSLVLNGYNEBPDPEPT 313
399 VDLCTYLOPLSGPGLPIKQVFHLSQTHGIRLGRYSIDKDSLVLNGYNEBPDPEPT 458
314 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSAATFNSTEGVLOHLR 373
459 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSAATFNSTEGVLOHLR 518
374 PLFOKSMGPFYLGCOLISLRPEKGAAGVDTTCYHDPVPGGLDIQQLYELSQLTH 433
519 PLFOKSMGPFYLGCOLISLRPEKGAAGVDTTCYHDPVPGGLDIQQLYELSQLTH 578
434 GTVQLGFYVLDRLSLFINGYAPQNLIRGEYOINFIHVMNLSNPPTSSEYITLLRDIO 493
579 GTVQLGFYVLDRLSLFINGYAPQNLIRGEYOINFIHVMNLSNPPTSSEYITLLRDIO 638
494 DKVTLTKGSQLHDTFRFCVLTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNLSFH 553
639 DKVTLTKGSQLHDTFRFCVLTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNLSFH 698
554 WLGSTYQVLDIHTHEMESVYQPTSSSSTQHFIYLNFTITNLPSQDKAQPCTINYOQNR 613
699 WLGSTYQVLDIHTHEMESVYQPTSSSSTQHFIYLNFTITNLPSQDKAQPCTINYOQNR 758
614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSL CNFSPILARRVDAIYEEF 673

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Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSLARRVDAIYEEF 818
Qy 674 LRMRNGTQLONFITLDRSSVLDGYFPNRPNEPLTGN 710
Db 819 LRMRNGTQLONFITLDRSSVLDGYFPNRPNEPLTGN 855

RESULT 11

US-09-884-441-312
; Sequence 312, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-441-312

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4,66-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFITNLRYEENMPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFITNLRYEENMPG 218
Qy 74 SRKNTTERVLOGLRLPKNSTVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGP 133
Db 219 SRKNTTERVLOGLRLPKNSTVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGP 278
Qy 134 GLDREQLYLBLSQTLHSITELGPTLDRDLSLYNGFTHRSSVPTTSGVSEEPFTLNF 193
Db 279 GLDREQLYLBLSQTLHSITELGPTLDRDLSLYNGFTHRSSVPTTSGVSEEPFTLNF 338
Qy 194 INNLRYADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRVIALRSVNGAETR 253
Db 339 INNLRYADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRVIALRSVNGAETR 398
Qy 254 VDLICTYLOPLSGGLPIKQVFNHLSQQTGIRLGPYSLDKDSL YLNGVNEPDPDEPT 313
Db 399 VDLICTYLOPLSGGLPIKQVFNHLSQQTGIRLGPYSLDKDSL YLNGVNEPDPDEPT 458
Qy 314 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLOYSPMGKSAFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLOYSPMGKSAFNSTEGVLOHLR 518
Qy 374 PLFQKSSMGFPYLGCOLISLRPEKGAATGVDTTCTHPRDPVPGGLDIQOLYMBLSQTLH 433
Db 519 PLFQKSSMGFPYLGCOLISLRPEKGAATGVDTTCTHPRDPVPGGLDIQOLYMBLSQTLH 578
Qy 434 GVTOLGTYVLDRLSLFNGYAPONLSIRGEYQINFHLYNNMLSNPDPSTSEYITLLRDIQ 493
Db 579 GVTOLGTYVLDRLSLFNGYAPONLSIRGEYQINFHLYNNMLSNPDPSTSEYITLLRDIQ 638
Qy 494 DKVTTLKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSLVQVFLDKTLNLSFH 553
Db 639 DKVTTLKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSLVQVFLDKTLNLSFH 698
Qy 554 WLGSYQVLDIHVTEMSSVYQPTSSSTQHFYLNFTITNLRYSDKAQPGTINYQNRK 613
Db 699 WLGSYQVLDIHVTEMSSVYQPTSSSTQHFYLNFTITNLRYSDKAQPGTINYQNRK 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSLARRVDAIYEEF 673

Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSLARRVDAIYEEF 818
Qy 674 LRMRNGTQLONFITLDRSSVLDGYFPNRPNEPLTGN 710
Db 819 LRMRNGTQLONFITLDRSSVLDGYFPNRPNEPLTGN 855

RESULT 12

US-09-884-441-478
; Sequence 478, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 478
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-478

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4,66-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFITNLRYEENMPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFITNLRYEENMPG 218
Qy 74 SRKNTTERVLOGLRLPKNSTVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGP 133
Db 219 SRKNTTERVLOGLRLPKNSTVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGP 278
Qy 134 GLDREQLYLBLSQTLHSITELGPTLDRDLSLYNGFTHRSSVPTTSGVSEEPFTLNF 193
Db 279 GLDREQLYLBLSQTLHSITELGPTLDRDLSLYNGFTHRSSVPTTSGVSEEPFTLNF 338
Qy 194 INNLRYADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRVIALRSVNGAETR 253
Db 339 INNLRYADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRVIALRSVNGAETR 398
Qy 254 VDLICTYLOPLSGGLPIKQVFNHLSQQTGIRLGPYSLDKDSL YLNGVNEPDPDEPT 313
Db 399 VDLICTYLOPLSGGLPIKQVFNHLSQQTGIRLGPYSLDKDSL YLNGVNEPDPDEPT 458
Qy 314 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLOYSPMGKSAFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLOYSPMGKSAFNSTEGVLOHLR 518
Qy 374 PLFQKSSMGFPYLGCOLISLRPEKGAATGVDTTCTHPRDPVPGGLDIQOLYMBLSQTLH 433
Db 519 PLFQKSSMGFPYLGCOLISLRPEKGAATGVDTTCTHPRDPVPGGLDIQOLYMBLSQTLH 578
Qy 434 GVTOLGTYVLDRLSLFNGYAPONLSIRGEYQINFHLYNNMLSNPDPSTSEYITLLRDIQ 493
Db 579 GVTOLGTYVLDRLSLFNGYAPONLSIRGEYQINFHLYNNMLSNPDPSTSEYITLLRDIQ 638
Qy 494 DKVTTLKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSLVQVFLDKTLNLSFH 553
Db 639 DKVTTLKGSQLDHTRFCLVTNLTMDSVLYTVKALFSSNLDPSLVQVFLDKTLNLSFH 698
Qy 554 WLGSYQVLDIHVTEMSSVYQPTSSSTQHFYLNFTITNLRYSDKAQPGTINYQNRK 613
Db 699 WLGSYQVLDIHVTEMSSVYQPTSSSTQHFYLNFTITNLRYSDKAQPGTINYQNRK 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSLARRVDAIYEEF 673

DB 759 NIEDALNOLFRNSISIKYSPDCOVSTFRSVPRHHTGVDSLGNFSPILARVDRVAIYEEF 818
QY 674 LRMTRNGTOLQNFPTLDRSSVLVDGYSPNNEPILTGN 710
DB 819 LRMTRNGTOLQNFPTLDRSSVLVDGYFPNNEPILTGN 855

RESULT 13
US-09-907-969-312
/ Sequence 312, Application US/09907969
/ Publication No. US20030091580A1
/ GENERAL INFORMATION:
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: King, Gordon E.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Piling, Steven P.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary Richard
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Hill, Paul
/ APPLICANT: Albone, Earl
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C8
/ CURRENT APPLICATION NUMBER: US/09/907, 969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 312
/ LENGTH: 914
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-312

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTSPASIFGSPAASHLLILFTLNFITNLRYEENMPG 73
DB 159 FTHRSSVSTSTPGTPTVYLGASKTSPASIFGSPAASHLLILFTLNFITNLRYEENMPG 218
QY 74 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 219 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 278
QY 134 GLDREOLYELISOLTHSITELGAPYTLDRDSL YVNGFTHRSSVPTTSGVVSSEPFITLNF 193
DB 279 GLDREOLYELISOLTHSITELGAPYTLDRDSL YVNGFTHRSSVPTTSGVVSSEPFITLNF 338
QY 194 INNLRYADMGOQPSLKFNTIDNVMKHLSPFORSSLGARYTGCRIYALRSVNGAETR 253
DB 339 INNLRYADMGOQPSLKFNTIDNVMKHLSPFORSSLGARYTGCRIYALRSVNGAETR 398
QY 254 VDLCTYLQPLSGQLPIKQVFHLSQOHTGIRLGPYSLDKDSL YVNGNEPDPDEPT 313
DB 399 VDLCTYLQPLSGQLPIKQVFHLSQOHTGIRLGPYSLDKDSL YVNGNEPDPDEPT 458
QY 314 TPKRATTFPLPLSBAATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
DB 459 TPKRATTFPLPLSBAATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 518
QY 374 PLFPKSSGPFYLGQOLSLRPEKOGATGVDTCTHYAPDVGGLDIQOLYELISOLTH 433
DB 519 PLFPKSSGPFYLGQOLSLRPEKOGATGVDTCTHYAPDVGGLDIQOLYELISOLTH 578
QY 434 GVTOLGPFYVLDRLSLFINGVAPONLSIRGEYQINFHIVNMNLSNPDPSTSEYITLRLDIQ 493
DB 579 GVTOLGPFYVLDRLSLFINGVAPONLSIRGEYQINFHIVNMNLSNPDPSTSEYITLRLDIQ 638

QY 494 DKVTTLYKGSQULHDFRFLVTNLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTINASH 553
DB 639 DKVTTLYKGSQULHDFRFLVTNLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTINASH 698
QY 554 WLGSTYQVLDIVHTEMESVYOPTSSSTQHYLANFTNLNLYSQDKAPGTTNORNR 613
DB 699 WLGSTYQVLDIVHTEMESVYOPTSSSTQHYLANFTNLNLYSQDKAPGTTNORNR 758
QY 614 NIEDALNOLFRNSISIKYSPDCOVSTFRSVPRHHTGVDSLGNFSPILARVDRVAIYEEF 673
DB 759 NIEDALNOLFRNSISIKYSPDCOVSTFRSVPRHHTGVDSLGNFSPILARVDRVAIYEEF 818
QY 674 LRMTRNGTOLQNFPTLDRSSVLVDGYSPNNEPILTGN 710
DB 819 LRMTRNGTOLQNFPTLDRSSVLVDGYFPNNEPILTGN 855

RESULT 14
US-09-907-969-478
/ Sequence 478, Application US/09907969
/ Publication No. US20030091580A1
/ GENERAL INFORMATION:
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: King, Gordon E.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Piling, Steven P.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary Richard
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Hill, Paul
/ APPLICANT: Albone, Earl
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C8
/ CURRENT APPLICATION NUMBER: US/09/907, 969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 478
/ LENGTH: 914
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-478

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTSPASIFGSPAASHLLILFTLNFITNLRYEENMPG 73
DB 159 FTHRSSVSTSTPGTPTVYLGASKTSPASIFGSPAASHLLILFTLNFITNLRYEENMPG 218
QY 74 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 219 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 278
QY 134 GLDREOLYELISOLTHSITELGAPYTLDRDSL YVNGFTHRSSVPTTSGVVSSEPFITLNF 193
DB 279 GLDREOLYELISOLTHSITELGAPYTLDRDSL YVNGFTHRSSVPTTSGVVSSEPFITLNF 338
QY 194 INNLRYADMGOQPSLKFNTIDNVMKHLSPFORSSLGARYTGCRIYALRSVNGAETR 253
DB 339 INNLRYADMGOQPSLKFNTIDNVMKHLSPFORSSLGARYTGCRIYALRSVNGAETR 398
QY 254 VDLCTYLQPLSGQLPIKQVFHLSQOHTGIRLGPYSLDKDSL YVNGNEPDPDEPT 313
DB 399 VDLCTYLQPLSGQLPIKQVFHLSQOHTGIRLGPYSLDKDSL YVNGNEPDPDEPT 458
QY 314 TPKRATTFPLPLSBAATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 373
DB 459 TPKRATTFPLPLSBAATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 518

QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSQUTH 433
| | | | |
DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSQUTH 578
| | | | |
QY 434 GVTQLGPFYVLDRLSLFINGYAPQNLISRGXYQINFHIVNNLSNPDPSTSEYITLLRDIO 493
| | | | |
DB 579 GVTQLGPFYVLDRLSLFINGYAPQNLISRGXYQINFHIVNNLSNPDPSTSEYITLLRDIO 638
| | | | |
QY 494 DKVTTLYKGSQLDHDFRCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 553
| | | | |
DB 639 DKVTTLYKGSQLDHDFRCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 698
| | | | |
QY 554 WLGSTYQVLDIHVTEMSSVYOPTSSSTQHFIYLNFTITNLPSYQDKAOPGTNYORNR 613
| | | | |
DB 699 WLGSTYQVLDIHVTEMSSVYOPTSSSTQHFIYLNFTITNLPSYQDKAOPGTNYORNR 758
| | | | |
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSPILARRVDRVAIYEEF 673
| | | | |
DB 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSPILARRVDRVAIYEEF 818
| | | | |
QY 674 LRMTNRGTQLQNFLLDRSSVYLDGYSPNRNEPLTGNS 710
| | | | |
DB 819 LRMTNRGTQLQNFLLDRSSVYLDGYSPNRNEPLTGNS 855
| | | | |

RESULT 15

US-09-827-271-312
; Sequence 312, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PR
; ORGANISM: Homo sapien
US-09-827-271-312

Query Match 92.9%; Score 3663; DB 3; Length 914;

Best Local Similarity 99.9%; Pred. No. 4.6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTIPASIFGPSASHLLILFTLNFTITNLRYEENMPG 73
| | | | |
DB 159 FTHRSSVSTSTPGTPTVYLGASKTIPASIFGPSASHLLILFTLNFTITNLRYEENMPG 218
| | | | |
QY 74 SRKNTTERVYQGLRLPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHARDPTGP 133
| | | | |
DB 219 SRKNTTERVYQGLRLPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHARDPTGP 278
| | | | |
QY 134 GLDREQLYELLSQUTHSITEGPTLDRDSLTVNGFTHRSVPTTSGVSEEPFTLNFT 193
| | | | |
DB 279 GLDREQLYELLSQUTHSITEGPTLDRDSLTVNGFTHRSVPTTSGVSEEPFTLNFT 338
| | | | |
QY 194 INNIRYADMGQPSLKFENITDNVKKHLSPLFORSSIGARYTGCRVIALRSVNGAETR 253
| | | | |
DB 339 INNIRYADMGQPSLKFENITDNVKKHLSPLFORSSIGARYTGCRVIALRSVNGAETR 398
| | | | |
QY 254 VDLICTYLOPLSGGLPIKOVFHELISOOTGITRLGYSILDKOSLYLVNGNEBGPDEPPT 313
| | | | |
DB 399 VDLICTYLOPLSGGLPIKOVFHELISOOTGITRLGYSILDKOSLYLVNGNEBGPDEPPT 458
| | | | |
QY 314 TPKPATFTPLPLSEATTAMGYHLKTLINFTISNLQYSPDMGKSATFNSTEGVLQHLR 373
| | | | |
DB 459 TPKPATFTPLPLSEATTAMGYHLKTLINFTISNLQYSPDMGKSATFNSTEGVLQHLR 518
| | | | |

QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSQUTH 433
| | | | |
DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSQUTH 578
| | | | |
QY 434 GVTQLGPFYVLDRLSLFINGYAPQNLISRGXYQINFHIVNNLSNPDPSTSEYITLLRDIO 493
| | | | |
DB 579 GVTQLGPFYVLDRLSLFINGYAPQNLISRGXYQINFHIVNNLSNPDPSTSEYITLLRDIO 638
| | | | |
QY 494 DKVTTLYKGSQLDHDFRCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 553
| | | | |
DB 639 DKVTTLYKGSQLDHDFRCLVTNLTMDSVLVYKALFSSNLDPSLVEQVFLDKTLNLSFH 698
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QY 554 WLGSTYQVLDIHVTEMSSVYOPTSSSTQHFIYLNFTITNLPSYQDKAOPGTNYORNR 613
| | | | |
DB 699 WLGSTYQVLDIHVTEMSSVYOPTSSSTQHFIYLNFTITNLPSYQDKAOPGTNYORNR 758
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QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSPILARRVDRVAIYEEF 673
| | | | |
DB 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLGNFSPILARRVDRVAIYEEF 818
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QY 674 LRMTNRGTQLQNFLLDRSSVYLDGYSPNRNEPLTGNS 710
| | | | |
DB 819 LRMTNRGTQLQNFLLDRSSVYLDGYSPNRNEPLTGNS 855
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Search completed: October 14, 2006, 04:09:19
Job time : 189 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 14, 2006, 04:06:25 : Search time 40 Seconds

(without alignments)
1484.879 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQPARRRARTKLFTHRSSV.....QKLISEBDLNMHTGHHHHH 748

Scoring table:

BLOSUM62

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3649	92.5	22152	US-10-544-944-1	Sequence 1, Appli
2	3642	92.3	1148	US-11-105-233-195	Sequence 155, App
3	3642	92.3	1148	US-11-226-554-129	Sequence 129, App
4	3642	92.3	1148	US-11-248-718-129	Sequence 129, App
5	182	4.6	33	US-11-134-871-1509	Sequence 1509, Ap
6	161.5	4.1	396	US-10-541-657-2	Sequence 2, Appli
7	161.5	4.1	396	US-11-327-896A-2	Sequence 2, Appli
8	158.5	4.0	288	US-10-545-557-48	Sequence 48, Appli
9	146	3.7	625	US-10-545-557-40	Sequence 40, Appli
10	136	3.4	542	US-11-056-355B-82537	Sequence 82537, A
11	136	3.4	605	US-11-056-355B-82536	Sequence 82536, A
12	136	3.4	609	US-11-056-355B-82535	Sequence 82535, A
13	132	3.3	774	US-11-123-682-34	Sequence 34, Appli
14	130	3.3	401	US-11-234-587-355	Sequence 355, App
15	130	3.3	401	US-11-234-482-15	Sequence 15, Appli
16	121.5	3.1	1475	US-10-527-100-33	Sequence 33, Appli
17	118.5	3.0	270	US-11-334-081-36	Sequence 36, Appli
18	117	3.0	21	US-11-332-088-2	Sequence 2, Appli
19	117	3.0	21	US-11-346-129-30	Sequence 30, Appli
20	114.5	2.9	211	US-11-334-081-14	Sequence 44, Appli
21	114.5	2.9	233	US-11-334-081-55	Sequence 55, Appli
22	114.5	2.9	273	US-11-334-081-40	Sequence 40, Appli
23	114	2.9	489	US-10-498-697-1	Sequence 1, Appli
24	113.5	2.9	539	US-11-123-692-37	Sequence 37, Appli
25	113.5	2.9	539	US-11-123-692-42	Sequence 42, Appli

ALIGNMENTS

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RESULT 1
US-10-544-944-1
; Sequence 1, Application US/10544944
; Publication No. US20060134120A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OR INVENTION: Multiple Marker Assay for Detection of Ovarian Cancer
; FILE REFERENCE: 11757.00880S0
; CURRENT APPLICATION NUMBER: US/10/544,944
; PRIOR APPLICATION NUMBER: PCT/CA2004/000281
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 22152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13877)..(13878)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13880)..(13880)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; NAME/KEY: misc feature
; LOCATION: (13887)..(13887)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
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; LOCATION: (13890)..(13891)
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; LOCATION: (13893)..(13893)
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; LOCATION: (13903)..(13903)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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3 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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11 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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43 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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46 LOCATION: (16015)..(16015)
47 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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50 LOCATION: (16017)..(16017)
51 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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54 LOCATION: (16021)..(16021)
55 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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57 NAME/KEY: misc feature
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73 NAME/KEY: misc feature

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; LOCATION: (16046)..(16046)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16051)..(16051)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature

Query Match      92.5%; Score 3649; DB 6; Length 22152;
Best Local Similarity 99.7%; Pred. No. 1e-263;
Matches 695; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 FTRSSVSTSTGTPTVYLGASKTPTASIFGPSASHLLILFTLNFTITNLRYEENWMPG 73
DB 21397 FTRSSVSTSTGTPTVYLGASKTPTASIFGPSASHLLILFTLNFTITNLRYEENWMPG 21456
QY 74 SRKFTTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDPTGP 133
DB 21457 SRKFTTERVLOGLRLPLFKNTSVGPLYSGSRLLTLRPEKGEATGVDAICTHRPDPTGP 21516
QY 134 GLDREQLYLELSQTLHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 21517 GLDREQLYLELSQTLHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 21576
QY 194 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSIGARYGCRVIALRSYKNGAETR 253
DB 21577 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSIGARYGCRVIALRSYKNGAETR 21636
QY 254 VDLICTYLOPLSGRGLPIKQVFHELSQLTHGIRLGPYSLDKDSLXYNGNEGPDEPPT 313
DB 21637 VDLICTYLOPLSGRGLPIKQVFHELSQLTHGIRLGPYSLDKDSLXYNGNEGPDEPPT 21696
QY 314 TPKPATFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSSTEGVLOHLR 373
DB 21697 TPKPATFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSSTEGVLOHLR 21756
QY 374 PLFOKSMGPFYGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQOLYWELSQTLH 433
DB 21757 PLFOKSMGPFYGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQOLYWELSQTLH 21816
QY 434 GVTQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVMNLSPDPSTSEYITLLRDIO 493
DB 21817 GVTQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVMNLSPDPSTSEYITLLRDIO 21876
QY 494 DKVTTLYKGSQLDHTRFCLVTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNASH 553
DB 21877 DKVTTLYKGSQLDHTRFCLVTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNASH 21936
QY 554 WLGSTYQLVDIHYTEMSSVYOPTSSSTQHFYLNFTITNLPSODKAQPGTNNYORNR 613
DB 21937 WLGSTYQLVDIHYTEMSSVYOPTSSSTQHFYLNFTITNLPSODKAQPGTNNYORNR 21996
QY 614 NIEDALNQLFRNSSISYSPDCOVSTFRSVPNRHHGVSLCNFSLARVDVAIYEER 673
DB 21997 NIEDALNQLFRNSSISYSPDCOVSTFRSVPNRHHGVSLCNFSLARVDVAIYEER 22056
QY 674 LRMTNGTQLQNTFLDRSSVLVDGYSPPNRNEPLTGN 710
DB 22057 LRMTNGTQLQNTFLDRSSVLVDGYSPPNRNEPLTGN 22093

RESULT 2
US-11-105-233-195
; Sequence 195, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
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; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-195

Query Match      92.3%; Score 3642; DB 7; Length 1148;
Best Local Similarity 99.6%; Pred. No. 4.6e-265;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTRSSVSTSTGTPTVYLGASKTPTASIFGPSASHLLILFTLNFTITNLRYEENWMPG 73
DB 393 FTRSSVSTSTGTPTVYLGASKTPTASIFGPSASHLLILFTLNFTITNLRYEENWMPG 452
QY 74 SRKFTTERVLOGLRLPLFKNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDPTGP 133
DB 453 SRKFTTERVLOGLRLPLFKNTSVGPLYSGSRLLTLRPEKGEATGVDAICTHRPDPTGP 512
QY 134 GLDREQLYLELSQTLHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 513 GLDREQLYLELSQTLHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 572
QY 194 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSIGARYGCRVIALRSYKNGAETR 253
DB 573 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSSIGARYGCRVIALRSYKNGAETR 632
QY 254 VDLICTYLOPLSGRGLPIKQVFHELSQLTHGIRLGPYSLDKDSLXYNGNEGPDEPPT 313
DB 633 VDLICTYLOPLSGRGLPIKQVFHELSQLTHGIRLGPYSLDKDSLXYNGNEGPDEPPT 692
QY 314 TPKPATFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSSTEGVLOHLR 373
DB 693 TPKPATFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKSATFNSSTEGVLOHLR 752
QY 374 PLFOKSMGPFYGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQOLYWELSQTLH 433
DB 753 PLFOKSMGPFYGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQOLYWELSQTLH 812
QY 434 GVTQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVMNLSPDPSTSEYITLLRDIO 493
DB 813 GVTQLGFYVLDRLSLFINGYAPONLSIRGEYQINFHIVMNLSPDPSTSEYITLLRDIO 872
QY 494 DKVTTLYKGSQLDHTRFCLVTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNASH 553
DB 873 DKVTTLYKGSQLDHTRFCLVTNLTMDSVLVTYKALFSSNLDPDLVEQVFLDKTLNASH 932
QY 554 WLGSTYQLVDIHYTEMSSVYOPTSSSTQHFYLNFTITNLPSODKAQPGTNNYORNR 613
DB 933 WLGSTYQLVDIHYTEMSSVYOPTSSSTQHFYLNFTITNLPSODKAQPGTNNYORNR 992
QY 614 NIEDALNQLFRNSSISYSPDCOVSTFRSVPNRHHGVSLCNFSLARVDVAIYEER 673
DB 993 NIEDALNQLFRNSSISYSPDCOVSTFRSVPNRHHGVSLCNFSLARVDVAIYEER 1052
QY 674 LRMTNGTQLQNTFLDRSSVLVDGYSPPNRNEPLTGN 710
DB 1053 LRMTNGTQLQNTFLDRSSVLVDGYSPPNRNEPLTGN 1089

RESULT 3
US-11-226-554-129
; Sequence 129, Application US/11226554
; Publication No. US20060147373A1
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Franz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
```

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; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1C1
; CURRENT APPLICATION NUMBER: US/11/226,554
; CURRENT FILING DATE: 2005-09-13
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 129
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-226-554-129

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Query Match 92.3%; Score 3642; DB 7; Length 1148;

Best Local Similarity 99.6%; Pred. No. 4,6e-265;

Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNTTINLRYEENMPG 73
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QY 74 SRKFNTTERVLQGLRLPLFNKTSVGLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 133
DB 453 SRKFNTTERVLQGLRLPLFNKTSVGLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 512
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QY 194 INNLRYADMGQPGSLKFNITDVMKGLSPLFORSSLGARYGCRVIALRSYNGAETR 253
DB 573 INNLRYADMGQPGSLKFNITDVMKGLSPLFORSSLGARYGCRVIALRSYNGAETR 632
QY 254 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGIRLDPYSIDKSLYANGNEPDPBPT 313
DB 633 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGIRLDPYSIDKSLYANGNEPDPBPT 692
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTINFTISNLQYSPMGKGSATFNSTEGVLQHLR 373
DB 693 TPKPATTFPLPSEATTAMGYHLKTLTINFTISNLQYSPMGKGSATFNSTEGVLQHLR 752
QY 374 PLFOKSSMGPFYLGQQLISLRPEKDGATGVDTCYHPDPVGPGLDIOQLYELSQLTH 433
DB 753 PLFOKSSMGPFYLGQQLISLRPEKDGATGVDTCYHPDPVGPGLDIOQLYELSQLTH 812
QY 434 GTVQLGPTVLDRLSLFNGYAPQNLSTRGYQINFNHVMNLSNPDPSTSEYITLLRDIO 493
DB 813 GTVQLGPTVLDRLSLFNGYAPQNLSTRGYQINFNHVMNLSNPDPSTSEYITLLRDIO 872
QY 494 DKYTLTKGSQLDHTFPCLVTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNLSFH 553
DB 873 DKYTLTKGSQLDHTFPCLVTNLTMDSVLYVYKALFSSNLDPSLVEQVFLDKTLNLSFH 932
QY 554 WLGSYVQVLDIHYTEMSSVYOPTSSSTOHPYFNFTITNLPSYQDRAQPGTINYQNRK 613
DB 933 WLGSYVQVLDIHYTEMSSVYOPTSSSTOHPYFNFTITNLPSYQDRAQPGTINYQNRK 992
QY 614 NIBDALNQLFRNSSIKSYFSDCOVSTRSPVNRHHTGVDSICNSPLARRVRAIYEEF 673
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QY 674 LRMTRNGTOLONFTLDRSSVYLDGYSPPRNEPPLTNS 710
DB 1053 LRMTRNGTOLONFTLDRSSVYLDGYSPPRNEPPLTNS 1089

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RESULT 4
US-11-248-718-129

; Sequence 129, Application US/11248718

; Publication No. US2006016097A1

; GENERAL INFORMATION:

; APPLICANT: Cairns, Belinda

; APPLICANT: Chen, Ruihuan

; APPLICANT: Frantz, Gretchen

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Koepfen, Hartmut

; APPLICANT: Phillips, Heidi S.

; APPLICANT: Polakis, Paul

; APPLICANT: Spencer, Susan D.

; APPLICANT: Smith, Victoria

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wu, Thomas D.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and

; TITLE OF INVENTION: Treatment of Tumor

; FILE REFERENCE: P5001R1 US

; CURRENT APPLICATION NUMBER: US/11/248,718

; CURRENT FILING DATE: 2005-10-11

; PRIOR APPLICATION NUMBER: US/10/177,488

; PRIOR FILING DATE: 2002-06-19

; PRIOR APPLICATION NUMBER: US 60/299,500

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: US 60/300,880

; PRIOR FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: US 60/301,880

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/304,813

; PRIOR FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: US 60/312,312

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: US 60/314,280

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: US 60/339,227

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/323,268

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US 60/336,827

; PRIOR FILING DATE: 2001-11-07

; Remaining Prior Application data removed - See file wrapper or PALM.

; NUMBER OF SEQ ID NOS: 154

; SEQ ID NO 129

; LENGTH: 1148

; TYPE: PRT

; ORGANISM: Homo Sapien

US-11-248-718-129

Query Match 92.3%; Score 3642; DB 7; Length 1148;

Best Local Similarity 99.6%; Pred. No. 4,6e-265;

Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNTTINLRYEENMPG 73
DB 393 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNTTINLRYEENMPG 452
QY 74 SRKFNTTERVLQGLRLPLFNKTSVGLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 133
DB 453 SRKFNTTERVLQGLRLPLFNKTSVGLYSGCRLLTLRPEKDGATGVDALCTHRPDPGP 512
QY 134 GLDREQLYELSQLTHSITELGPTTLDRLSLYNGFTHRSSVPTSTGVVSEBPTLNT 193
DB 513 GLDREQLYELSQLTHSITELGPTTLDRLSLYNGFTHRSSVPTSTGVVSEBPTLNT 572
QY 194 INNLRYADMGQPGSLKFNITDVMKGLSPLFORSSLGARYGCRVIALRSYNGAETR 253
DB 573 INNLRYADMGQPGSLKFNITDVMKGLSPLFORSSLGARYGCRVIALRSYNGAETR 632
QY 254 VDLICTYLOPLSGRGLPIKQVFHLSQOHTGIRLDPYSIDKSLYANGNEPDPBPT 313

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Db      633 VDLCTYLQPLSGPGLPIKQVHELSQOTGHTIRLAGEYSIDKDSLYINGNEPGLDDEPPT 692
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Qy      374 PLFOKSSMGPFYLGQCLISLRPEKDGATGVDTCYHPDPVGEGLDIQOLYMWELSQLTH 433
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Qy      434 GTVQLGFFVLDRLSFLINGYAPQNLISIRGEYQINFMHVNMLSNPDPTSEYITLLRDIQ 493
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Qy      494 DKYTLTKSGQLDTPFCVLTNLTMSVLYVYKALFSSNLDPBLVQVFLDKTLNLSFH 553
        873 DKYTLTKSGQLDTPFCVLTNLTMSVLYVYKALFSSNLDPBLVQVFLDKTLNLSFH 932
Qy      554 WLGSTYQVLDIHTEMESSYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
        933 WLGSTYQVLDIHTEMESSYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 992
Qy      614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLQNFSPPLARRVDRAIYEEF 673
        993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLQNFSPPLARRVDRAIYEEF 1052
Db      674 LRMTNGTQLONFLLDRSSVLYVGYSPNRNEPLTGN 710
        1053 LRMTNGTQLONFLLDRSSVLYVGYSPNRNEPLTGN 1089

```

```

RESULT 5
US-11-134-871-1509
; Sequence 1509, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1509
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-1509

```

```

Query Match      4.6%; Score 182; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      582 TQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 614
        1 TQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 33

```

```

RESULT 6
US-10-541-657-2
; Sequence 2, Application US/10541657
; Publication No. US20060217379A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Robert M.
; APPLICANT: Semple, Graeme
; APPLICANT: Fioravanti, Beatriz
; APPLICANT: Pereira, Guilherme
; APPLICANT: Calderon, Inelda
; APPLICANT: Uy, Jane

```

```

; APPLICANT: Duvvuri, Kameshwari
; APPLICANT: Choi, Jin Sun Karoline
; APPLICANT: Xiong, Yifeng
; APPLICANT: Vibha, Dave
; TITLE OF INVENTION: 1,2,3-TRISUBSTITUTED ARYL AND HETEROARYL DERIVATIVES AS
; TITLE OF INVENTION: MODULATORS OF METABOLISM AND THE PROPHYLAXIS AND TREATMENT OF
; FILE REFERENCE: 34 US, PCT
; CURRENT APPLICATION NUMBER: US/10/541,657
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: US 60/440394
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/449,829
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/453,390
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/470,875
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-541-657-2

```

```

Query Match      4.1%; Score 161.5; DB 6; Length 396;
Best Local Similarity 72.7%; Pred. No. 0.0003;
Matches 32; Conservative 1; Mismatches 8; Indels 3; Gaps 1;

```

```

Qy      708 GNSADIQHSGRSSLEGPRFEQKLISEEDLNM---HTGHHHHH 748
        353 GNSADIQHSGRSSLEGPRFEQKIPNPLGLDSTRGHHHHH 396

```

```

RESULT 7
US-11-327-896A-2
; Sequence 2, Application US/11327896A
; Publication No. US20060155128A1
; GENERAL INFORMATION:
; APPLICANT: Arena Pharmaceuticals, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Lehmann, Juerg
; APPLICANT: Wong, Amy Siu-ting
; APPLICANT: Hurst, David
; APPLICANT: Shin, Young-Jun
; TITLE OF INVENTION: SUBSTITUTED PYRIDINYL AND PYRIMIDINYL DERIVATIVES AS MODULATORS
; TITLE OF INVENTION: OF METABOLISM AND THE TREATMENT OF DISORDERS RELATED THERETO
; FILE REFERENCE: 101 US2, REG
; CURRENT APPLICATION NUMBER: US/11/327,896A
; CURRENT FILING DATE: 2006-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-327-896A-2

```

```

Query Match      4.1%; Score 161.5; DB 7; Length 396;
Best Local Similarity 72.7%; Pred. No. 0.0003;
Matches 32; Conservative 1; Mismatches 8; Indels 3; Gaps 1;

```

```

Qy      708 GNSADIQHSGRSSLEGPRFEQKLISEEDLNM---HTGHHHHH 748
        353 GNSADIQHSGRSSLEGPRFEQKIPNPLGLDSTRGHHHHH 396

```

```

RESULT 8
US-10-545-557-48
; Sequence 48, Application US/10545557
; Publication No. US20060222654A1
; GENERAL INFORMATION:

```

```

; APPLICANT: ANOSYS
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR RAISING ANTIBODIES AND FOR SCREENING AN
; TITLE OF INVENTION: REPERTOIRES
; FILE REFERENCE: 3665-158
; CURRENT APPLICATION NUMBER: US/10/545,557
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: PCT/IB2004/000888
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US60/447,291
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 48
; LENGTH: 288
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: LS-GFP-Myc/His
; US-10-545-557-48

Query Match          4.0%; Score 158.5; DB 6; Length 288;
Best Local Similarity 24.6%; Pred. No. 0.00032;
Matches 81; Conservative 30; Mismatches 111; Indels 107; Gaps 14;

QY 443 LDRDSLFGINGVAPONLSIRGEYQ-----INPHIVNMNLSNPDPTSEYITLIRDIQ 493
DB 44 LGGD---VNGH---KFSVSGEGSGDATYGLTLKFICTTGKLPVMPPT----- 85
QY 494 DRYTTLTKYSQSL-----HDTFRFLCLVNLITMDSVLVYKALFSSNLDPSLVEQVF 543
DB 86 -LVTTLVGVQCFSRYPDRHMKQIDFPK-----SAPBEGYVERITTF-----F 126
QY 544 LD-----KTLNASHPMWIGSTYQLVDIHVTEMESGVYOPTSSSTQHFYLNFTITNLPYSOD 599
DB 127 KDDGNKTK-RAEYKFEIGDTL---VNRILKGIDEFEDGNILGHKLEVYNNSHNYIMAD 181
QY 600 KAPGTNNYORNRKNTIEDALNOLFRNSISIKSYFSDQVSTFRSVPNRHHTGVDSLGNFSP 659
DB 182 KQNGKIKANFKIRHNIEDGSVGLADHYQQNTPIGDPFV---LLPNHYLSTQSALSKDP 237
QY 660 LARVRVVAIYEELFMTKTRNGTOLQNTFLDRSSVLVDGYSPPNNEPLTGNADIQHSGGR 719
DB 238 NEKRDMHVVLL--EF--VTAGITL-----GM 259
QY 720 SSLGPRFEOKLISEEDLNMTGHHHHH 748
DB 260 DELYKPRFEOKLISEEDLNMTGHHHHH 288

RESULT 9
US-10-545-557-40
; Sequence 40, Application US/10545557
; Publication No. US20060222654A1
; GENERAL INFORMATION:
; APPLICANT: ANOSYS
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR RAISING ANTIBODIES AND FOR SCREENING AN
; TITLE OF INVENTION: REPERTOIRES
; FILE REFERENCE: 3665-158
; CURRENT APPLICATION NUMBER: US/10/545,557
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: PCT/IB2004/000888
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US60/447,291
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 40
; LENGTH: 625
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: LS-GFP-C1/C2
; US-10-545-557-40
```

```

Query Match          3.7%; Score 146; DB 6; Length 625;
Best Local Similarity 19.2%; Pred. No. 0.0086;
Matches 124; Conservative 67; Mismatches 178; Indels 276; Gaps 31;

QY 191 NFTINLRVYADWQPSGLKFNITDNYMKILLSPFORSSIGARYTGCRVIALSVKNGA 250
DB 170 NYNSHNHYIMADK-QKXGDKTKNFK---IRH-----NIEDGS 201
QY 251 ETRVDLLCTYIQ--PLSGPGLPIKQVHELSQOT-----HGITRLGPGYS 292
DB 202 ---VOLADHYQQNTPI-GDGPVLLPDNHYLSTQSALSKDPNEKRDHVVLEFVTAAG-IT 256
QY 293 LDKDSLVIANGYNREGDPDPTTPKATFLPLPSATAMGY---HLKTLT-----NF 343
DB 257 LGMDLEYLR-----PPSYCTCLKGYAGNHCCTKCVPELGMNG 295
QY 344 TISNLQSPDMQKSGATPSTEGVLQHLRLPLFOKSMGPPYLGQ-----LISLRPKD 398
DB 296 NIANSQIA-----ASSVTVTFGLQHWVPELARLN----- 325
QY 399 GAATGVDTTCYHPDPVPGGLDIQOL--YWEISQUTHGVTOGLFYVLDRLDSLFGINGVAPQ 456
DB 326 --RAGMVAAMTPSSNDNPMIQVNLRRMMVTVGVVTOGASRLASHEYLR----- 372
QY 457 NLSIGETQINPH-----IYNNNLSN-----PDPTSSRYITLIRDIQK 495
DB 373 --AFVVAISLNGHEPFDIHDVKKKKEFEVGNKKNAHVNLFEETVEAOYVRLYPTSGHT 430
QY 496 VTTL---YKGSQLDHDTFRFLCVTLNLTMDSVLVTVKA-----LFSSNLDPSLVEQVF 544
DB 431 ACTLRFELLGCELNGCANPLGKNNISIPDKQITASSSYKTMGLHFSNN--PSYAR---L 485
QY 545 DKTNLASFHWIGSTY---QVLDIHV---TEWESSYVQPTSSSTQHFYLNFTITNLPYSQ 598
DB 486 DKQGNFN-AMVAGSYGNQDMLQVLDGSSKEVGIITQGARNGSVQFVASYRVA---YSN 541
QY 599 DKAQ-----PGTNNYORNRKNTIEDALNOLFRNSISIKSYFSDQVSTFRSVP 643
DB 542 DSANWTEYODPRTGSKTFFGNNMNSHKN-----LFETPIRLARY-----VRL 586
QY 644 PRHHTGVDSLGNFSLARVRVAIYEELFMTKTRNGTOLQNTFLDRSSVLVDGYSPPNN 703
DB 587 PYAMH-----NRIALRLLELGC----- 603
QY 704 EPLTGNADIQHSGGRSSLGPRFEOKLISEEDLNMTGHHHHH 748
DB 604 -----FEOKLISEEDLNMTGHHHHH 625

RESULT 10
US-11-056-355B-82537
; Sequence 82537, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO: 82537
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1) - (542)
; OTHER INFORMATION: Ceres Seq. ID no. 12666070
```

US-11-056-355B-82537

Query Match 3.4%; Score 136; DB 7; Length 542;

Best Local Similarity 20.6%; Pred. No. 0.039;

Matches 99; Conservative 67; Mismatches 185; Indels 130; Gaps 20;

113 KDGATGVDAICTHRPDPGGLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHR 172
DB RDEEVQG-DTVIERND-----QSKLETAKL-----RIYQWIDVNLRSSEYTEN 134
173 SSVPTTSGVASEEPTLNTFTNNLRVYADMGQPSGL-KFNITDNVMKHLPLPFGRSS- 230
DB SRIPTMKFGTAKDADFRRDLTINSLFYNNINGAVEDLTERGIDDLKSGKITVPLPAKATF 194
231 -----LGAATGCRVIALRSVNGAETRYDLCITYLOPLSGGLPIKQVFHEL 278
DB 195 LDDPLRLVLAVERFGARFGFTLDEELKEAASSEEVVAL-----GKISRERIGNEI 245
QY 279 SQQTG-----ITRLGPTSLDKSLYLNGVNEPDPDE-----PTTPKP 317
DB 246 DLMISGNPVSATVTLSDKLFSVVPALPSSAEPSPENCGLSSQYLEAMMSLKTTPR 305
QY 318 -----ATFLP-----PLSEATTAMGYHLK 337
DB 306 GKFSGEQRRLALYAAAFLEPFRKTVYKDTGKSIPIVNNHIFKFSMKRKTSDAETVNNIHQT 365
QY 338 TLTNFTTSLNLOYSRDMGKGSATFNSTGVLQH-----LRLPLFOKSGMPYLGCOLIS 392
DB 366 TERFRLIPSLLEVKKDVLEDELTLW--AADILEHMKSTLNDPVIPTATSKIRVLTG---FL 420
QY 393 LRPEKD-----GAATGVDTCYHPDPVGPGLDIQOLYWELSQL--THGVTOLGPFYVLD 446
DB 421 LNDIDFMRVSLTSLTSLSATV--DGSNDHODIGQLDFQLERMRETYLTVEATTIHELGLD 478
QY 447 SLF-----INGYAPONLS-IRG-----EYQINFHIVMNLSPPTSESYITLLRDID 494
DB 479 KIMDAKPLVNGREIMQIAELKSGSLIRWQOK--LITWOLAVPNTAECEKEMWRDIXA 536
QY 495 K 495
DB 537 K 537

RESULT 11

US-11-056-355B-82536

; Sequence 82536, Application US/11056355B

; Publication No. US20060150283A1

; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav

; APPLICANT: Alexandrov, Nickolai

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

; FILE REFERENCE: 2750-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056,355B

; PRIOR FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544,190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 82536

; LENGTH: 605

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)..(605)

; OTHER INFORMATION: Ceres Seq. ID no. 12666069

US-11-056-355B-82536

Query Match 3.4%; Score 136; DB 7; Length 605;
Best Local Similarity 20.6%; Pred. No. 0.046;
Matches 99; Conservative 67; Mismatches 185; Indels 130; Gaps 20;

113 KDGATGVDAICTHRPDPGGLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHR 172

DB 152 RDEEVQG-DTVIERND-----QSKLETAKL-----RIYQWIDVNLRSSEYTEN 197

QY 173 SSVPTTSGVASEEPTLNTFTNNLRVYADMGQPSGL-KFNITDNVMKHLPLPFGRSS- 230

DB 198 SRIPTMKFGTAKDADFRRDLTINSLFYNNINGAVEDLTERGIDDLKSGKITVPLPAKATF 257

QY 231 -----LGAATGCRVIALRSVNGAETRYDLCITYLOPLSGGLPIKQVFHEL 278

DB 258 LDDPLRLVLAVERFGARFGFTLDEELKEAASSEEVVAL-----GKISRERIGNEI 308

QY 279 SQQTG-----ITRLGPTSLDKSLYLNGVNEPDPDE-----PTTPKP 317

DB 309 DLMISGNPVSATVTLSDKLFSVVPALPSSAEPSPENCGLSSQYLEAMMSLKTTPR 368

QY 318 -----ATFLP-----PLSEATTAMGYHLK 337

DB 369 GKFSGEQRRLALYAAAFLEPFRKTVYKDTGKSIPIVNNHIFKFSMKRKTSDAETVNNIHQT 428

QY 338 TLTNFTTSLNLOYSRDMGKGSATFNSTGVLQH-----LRLPLFOKSGMPYLGCOLIS 392

DB 429 TERFRLIPSLLEVKKDVLEDELTLW--AADILEHMKSTLNDPVIPTATSKIRVLTG---FL 483

QY 393 LRPEKD-----GAATGVDTCYHPDPVGPGLDIQOLYWELSQL--THGVTOLGPFYVLD 446

DB 484 LNDIDFMRVSLTSLTSLSATV--DGSNDHODIGQLDFQLERMRETYLTVEATTIHELGLD 541

QY 447 SLF-----INGYAPONLS-IRG-----EYQINFHIVMNLSPPTSESYITLLRDID 494

DB 542 KIMDAKPLVNGREIMQIAELKSGSLIRWQOK--LITWOLAVPNTAECEKEMWRDIXA 599

QY 495 K 495

DB 600 K 600

RESULT 12

US-11-056-355B-82535

; Sequence 82535, Application US/11056355B

; Publication No. US20060150283A1

; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav

; APPLICANT: Alexandrov, Nickolai

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

; FILE REFERENCE: 2750-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056,355B

; PRIOR FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544,190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 82535

; LENGTH: 609

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)..(609)

; OTHER INFORMATION: Ceres Seq. ID no. 12666068

US-11-056-355B-82535

Query Match 3.4%; Score 136; DB 7; Length 609;
Best Local Similarity 20.6%; Pred. No. 0.047;
Matches 99; Conservative 67; Mismatches 185; Indels 130; Gaps 20;

113 KDGATGVDAICTHRPDPGGLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHR 172
DB 156 RDEEVQG-DTVIERND-----QSKLETAKL-----RIYQWIDVNLRSSEYTEN 201
QY 173 SSVPTTSGVASEEPTLNTFTNNLRVYADMGQPSGL-KFNITDNVMKHLPLPFGRSS- 230
DB 202 SRIPTMKFGTAKDADFRRDLTINSLFYNNINGAVEDLTERGIDDLKSGKITVPLPAKATF 261


```

Db      311 VRFLKTSNRAELRG--LKRGAASYLVQVRARSEAGYGFPGQEHHSQTQLDESEGWREGG 368
QY      719 RSSLEGPRFEQKLISEEDLNM---HTGHHHHH 748
Db      369 RSSLEGPRFEQKLI PNPLGLDSTRGTGHHHHH 401

```

RESULT 15

```

US-11-234-482-15
; Sequence 15, Application US/11234482
; Publication No. US20060204512A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: G11, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P01-004
; CURRENT APPLICATION NUMBER: US/11/234,482
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/612,488
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ. ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B4-CF2
US-11-234-482-15

```

```

Query Match      3.3%; Score 130; DB 7; Length 401;
Best Local Similarity 32.7%; Pred. No. 0.072;
Matches 50; Conservative 12; Mismatches 53; Indels 38; Gaps 8;

```

```

QY      632 FSDCQVSTFRSVP-----NRHHTGVDSL CNFSPLARR--VDRVAIYEE----- 672
Db      251 FEPPVNTTDRVPAVSDIRVTRSSPSSLTAWAVPRAPSGAWLDYEVKYEKGAEQPS 310
QY      673 --FLKMTNRNGTQUNFTLDR-SSVLYD-----GYSF---NRNEPLTGNADIQHSGG 718
Db      311 VRFLKTSNRAELRG--LKRGAASYLVQVRARSEAGYGFPGQEHHSQTQLDESEGWREGG 368
QY      719 RSSLEGPRFEQKLISEEDLNM---HTGHHHHH 748
Db      369 RSSLEGPRFEQKLI PNPLGLDSTRGTGHHHHH 401

```

Search completed: October 14, 2006, 04:10:05
 Job time : 43 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2006, 03:59:20 ; Search time 46 Seconds
(without alignments)
1564.568 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQPARARARLFTFRSSV.....OKLISEDDLNMTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	144.5	3.7	1408	2 H69068	cell surface glyco
2	135.5	3.4	1117	2 S63399	probable membrane
3	123.5	3.1	2477	2 S14428	fibronectin precu
4	122	3.1	631	2 I52257	episialin - mouse
5	121.5	3.1	1475	2 S42718	nuclear pore compl
6	121.5	3.1	2471	2 T42977	large tegument pro
7	121.5	3.1	5005	2 F82884	hypothetical prote
8	121	3.1	1131	2 T41144	hypothetical serin
9	118	3.0	532	2 T34235	hypothetical prote
10	117.5	3.0	1377	2 A38926	DNA-binding protei
11	116	2.9	1848	2 A44140	cellulose-binding
12	115.5	2.9	1474	2 F69009	probable membrane
13	115	2.9	888	2 A54280	cell differentiat
14	114.5	2.9	709	2 A53364	carcinoembryonic a
15	113.5	2.9	855	2 T07015	Cf-4A protein - to
16	113.5	2.9	1004	2 B25039	outer cell wall pr
17	113.5	2.9	1369	2 T17504	hypothetical prote
18	113.5	2.9	3344	2 UQ1899	genome polypeptid
19	113.5	2.9	5762	2 A41819	proline-rich pepi
20	112.5	2.9	838	2 S38156	hypothetical prote
21	112.5	2.9	948	2 T11678	hypothetical prote
22	112.5	2.9	1348	2 AH1115	cell surface prote
23	112.5	2.9	4936	2 AH2515	hypothetical prote
24	112	2.8	643	2 S55593	membrane protein S
25	112	2.8	3587	2 T31075	tyrocidine synthet
26	111.5	2.8	919	2 S45889	probable regulator
27	111.5	2.8	1622	2 AE1717	probable cell surf
28	111	2.8	1777	2 T34369	hypothetical prote
29	111	2.8	2386	1 FNHU	fibronectin precu

30	110.5	2.8	630	2 A39344	tumor-associated m
31	110.5	2.8	1778	2 J70382	apolipoprotein B -
32	110.5	2.8	2508	2 S61441	surface-associated
33	110	2.8	628	1 A39262	transcription fact
34	110	2.8	1128	2 A49960	bud emergence prot
35	110	2.8	1349	2 A11476	cell surface prote
36	110	2.8	3131	2 T39553	vacuolar protein s
37	109.5	2.8	1268	1 A39640	neural cell adhesi
38	109	2.8	989	2 T56333	apolipoprotein B -
39	109	2.8	998	2 C75489	conserved hypothet
40	108.5	2.8	500	2 D97302	hypothetical prote
41	108.5	2.8	504	2 T33485	hypothetical prote
42	108.5	2.8	537	2 A35400	surface protein T6
43	108.5	2.8	776	2 A82787	TonB-dependent rec
44	108.5	2.8	1040	2 D86568	protein ZK757.3 (1
45	108.5	2.8	1113	2 H84105	hypothetical prote

ALIGNMENTS

RESULT 1

H69068
cell surface glycoprotein (8-layer protein) related protein - Methanobacterium thermoaut
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69068
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Accession: H69068
A:Molecule type: DNA
A:Residues: 1-1408 <MTH>
A:Cross-references: UNIPROT:O27557; UNIPARC:UP1000006761; GB:AE000911; GB:AE000666; NID
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1513
A:Start codon: TTG

Query Match	3.7%	Score 144.5	DB 2	Length 1408	Best Local Similarity 20.1%	Pred. No. 0.19	Matches 157	Conservative 99	Mismatches 258	Indels 269	Gaps 40
QY	58	NETITNLRYEENMMGSKKFTT---	ERYVGLRLPLFKNTSVGLYSGCRLTLIRPKD	114							
DB	444	NFTVT-----PDACKKVLTLGSDGLTRFPFIISNLSVPL-----		480							
QY	115	GEAGVDAICTRRPPPGGLDRQLYLEL-SQTHSTTEGPTYLDSDSYLVNGFTHS	173								
DB	481	-----NGICP-----LVYTLRGNTTNGDSGTWRLD---LYINGY--RT	515								
QY	174	SVPTSTGVSEEPFTLFTI-----	NNLRVADNGQ	205							
DB	516	AGKWEVGSLETFEEFEYTLRNSRAVSGVNNPPATVRFGLPLIRPMILRVTPSGQ	575								
QY	206	PGSLKFNITDVMGHLSPLQFRSSLGARYGCIVIALRSYKNAETRV-----	254								
DB	576	E-PLKVVNTADVNGDLPDSYTEL---YIDGVILDSRVNTVNAASRTTVSFNRTLAAG	631								
QY	255	--DLICTVLP-----LSGFLPIKOVFHELSQOTHG-----ITRL--GPSYLDK	295								
DB	632	LYETINDLEPLVYVWEGEKFTLEN--FTLTPSGAALPLTVYSAMITINDSNRSTYA	689								
QY	296	DSLVLNG-----YNEPGDEPPTPKPATFPLPLSEATITANGYH---LKTILT-LNF	343								
DB	690	-TIVNGVPDHTKVLNIPGES---TVPFSTSLPLDGLYTIISNNVSGTVRVLSANF	745								
QY	344	TISLQVSPDMGKSAIFNSTEGVLQHILRLRFLPKSSMGPRVYLCQLISLRPEKGATG	403								

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Db      746 TLSNVTSPVEKSPINVTVAIV-----RNGDLAG 777
Qy      404 VDTTCYHPDPVPGGLDIQOLYWEISQLTHGVTOLGPFYLDRLSLINGAPONLSIRG 463
Db      778 -DPAVLLYLDVA-----METRTVS-----VPGKSVLVS--FKELAPGE 816
Qy      464 YQINFIH---VNMNLSNPDPTSSSEYITLRLDIOQKVTLLKGSQGLDTPFACL-VTN--- 516
Db      817 YRLRLSGTDTVTIRVLEPDTITGF-----NTPVTPAPL--SVASLANTNPHD 865
Qy      517 -----LMDSVLYTVKALFSSNLDPSLVEQVFLDKTNASFWMLG----- 556
Db      866 LVIGETARLWDDGVVVENIV--SLSPGETRELAAGTLLPGHVTGINSFKIVAVLR 922
Qy      557 -STYQVLDIVHTEMESSVYOP-----TSSSSTOHFIYNT---TNLPISQKAPGT 605
Db      923 PASITLSDLRAT--PSSGSPFLITATATANTGEVDGNVAVLYINGLAVDEKNTVGA 980
Qy      606 TNYQRNKNIEDALNOLFRNSI-----KSYFSDCOVSTFRSVP---NRHHT 649
Db      981 -----GRSVQVAFNHTIENAGIYLAGISLTPLDVRLSEPAISNLATPLTGVSPHRI 1034
Qy      650 GVDLSLGNSS-----PLARRVDRVAIYEBFLAMTRNGTOLQNTLDRS-----SVLVDG 697
Db      1035 IVTALVSTTERSGSNYTAGLYIDGVNVQNRIVRYTGPSSVLVSFTADISEPGEHQVTNS 1094
Qy      698 YSP 700
Db      1095 LSP 1097

```

RESULT 2

663399
 probable membrane protein YNR067C - Yeast (Saccharomyces cerevisiae)
 N/A: alternate names: hypothetical protein N3547
 C/Species: Saccharomyces cerevisiae
 C/Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 C/Accession: S63399
 R/Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, April 1996
 A/Reference number: S62944
 A/Accession: S63399
 A/Molecule type: DNA
 A/Residues: 1-1117 <DURS>
 A/Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:Z71682; NID:G1302597; P1
 A/Experimental source: strain S288C
 C/Genetics:
 A/Gene: MIPS:YNR067C
 A/Cross-references: SGD:S0005350
 A/Map position: 14R
 C/Keywords: transmembrane protein
 F/6-22/Domain: transmembrane #status predicted <TM>

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Query Match      3.44; Score 135.5; DB 2; Length 1117;
Best local similarity 21.14; Pred. No. 0.56; 255; Indels 233; Gaps 39;
Matches 156; Conservative 94; Mismatches 255;
Qy      4 PARARATKLFTHRSSVSTSTPGTPYVIGA-----SKTPAS--IFGSAASHL 51
Db      206 PSYSSQETKIIP--SLTSNKITITIVRTMAATAGDSFIACSTLPASSSTLFPYNSGTOP 263
Qy      52 LILFTLFTTNILNLYEEN-----MMPGSRKNTTERV-----LOGLLRPL 91
Db      264 LVQ-TLASTSTSPAVPSNRQTITLSPSVLSTTSPYPSNITENGSSPSPSLSTVSPV 322
Qy      92 FKNTSVGPVLYSGCKRLTLRPEKGEATVNDALCTHRPPPTPGGLDRQLYELLS-QLTHS 150
Db      323 YPSSSTGNIL-----LSSLFSTVDSSS-----PVSGTLDD--TIYSSSMQATIS 365
Qy      151 ITELGPYLLDLSLVNFTHRSSVPTSTGVSEFPPLTNFTTNILRYMADMGQPSGLK 210
Db      366 SSSSSRQTKTSSS-----SLSTSTSTATTNTSSST--TIYNLNAVSTDEPPTV- 414

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Qy      211 FNITDWMKHLSPLEFORSSLGARTGCVIALRSYKNGAETRVLDLCTYQLPSLGGPGL 270
Db      415 FDRSPNPM-----SLADSVN-----DGP-IQ 435
Qy      271 IKQVFEHL--SQOTHGTRILGYSLDK-----DSLVLNGVNEPGEDEEP 312
Db      436 TNKFYTNLVGSGESAPF--VYPYSLMKYTSSSGYPAVOHTTVDOYSYGYSGSSGNAEYL 493
Qy      313 TTPKPATFPLPPLSEATYAMGHYLLKTLTNFTSNLIQSPDMOKGSATFNSTEGVL----- 368
Db      494 VNP-----LGIAHVFSASNPDSSMTWQVDEMTLSTTVLSSESN 533
Qy      369 ---QHILRPLFKSSMGPFLYGQLSLRPREKGAATGVDTCTYHPDPVPGGLDIQOLY 425
Db      534 DSSNYLEIPLVQ--GNG-FATGYIYHSLN-AKIGSSVGFNTIYSSSSNLAQGI-----LK 585
Qy      426 WEISQLTHGVTOLGPFYLDRLSLFINGAPONLSIRGEYOINRH-----IYNMNLSNP 479
Db      586 YRIT-LINGVTWL-CYIIGPDDLSTDF--SLEVSSEYEIKASAVDGLIQLAVA-PG 639
Qy      480 PTSSE-----YIT-LLRDIQKVTTLTK-----GQOL-----HDTFR 510
Db      640 ETDYEVFYDQAGMYVTNPFKLGVSDDSTAYTEFSYTTQESASGSTMTIRALPHHSSFS 699
Qy      511 FCLVTNLMDSVLTVYKALFSSNLDPSLVEQVFLDKTNASFWMLGSTYQ----- 560
Db      700 DIMQDYVTGIGLAASTTGVMNGYLTSLQ-----FSTSLNQISLWPLPSSQLGSLNLEYSK 755
Qy      561 -----LYDIIHTEMESSVYQPTSSSSTOHFIYNTFNLPY-----SODKAPGTIN 607
Db      756 EQLQLAEVANSSEIQVSISSISGLNT--YLVGVIDKYSYILLTVSEIILIDKASTYST- 812
Qy      608 YQRNKNIEDALNOLFRN 625
Db      813 ----LENIKSAFDILQN 826

```

RESULT 3

S14428
 fibronectin precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
 C/Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
 R/Hynes, R.O.
 submitted to the EMBL Data Library, July 1989
 A/Reference number: S14428
 A/Accession: S14428
 A/Molecule type: mRNA
 A/Residues: 1-2477 <HYN>
 A/Cross-references: UNIPROT:P04937; UNIPARC:UPI000012A7G6; EMBL:X15906; NID:G56163; P1DN
 R/Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
 EMO J. 6, 2573-2580, 1987
 A/Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
 A/Reference number: S12455; MUID:88054951; PMID:2445560
 A/Accession: S12455
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 609-1810,'T',1812-2283 <SCH>
 A/Cross-references: UNIPARC:UPI0000177AB; EMBL:X15906
 R/Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
 A/Title: A single rat fibronectin gene generates three different mRNAs by alternative splicing.
 A/Reference number: A22319; MUID:84238097; PMID:6089177
 A/Accession: A22319
 A/Molecule type: DNA
 A/Residues: 2052-2237 <TM>
 A/Cross-references: UNIPARC:UPI0000177AB
 R/Falkenberg, C.; Englund, J.U.; Thøgersen, I.B.; Salvesen, G.; Akerström, B.
 Biochem. J. 301, 745-751, 1994
 A/Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex 1
 A/Reference number: S46203; MUID:94330948; PMID:7519849
 A/Accession: S46203
 A/Status: preliminary

A.Molecule type: protein
A.Residues: 1193-1192,'GN',1268,'P',1270-1271,'D',1273,'CG',1276,'PY',1385-1399 <FAL>
A.Cross-references: UNIPARC:UPI0000177AEC; UNIPARC:UPI0000177AEE
R.Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A.Title: Organization of the fibronectin gene provides evidence for exon shuffling during
A.Reference number: S00459; MUID:88054950; PMID:3119323
A.Accession: S00459
A.Molecule type: DNA
A.Residues: 1-139,'382-2477 <PAT>
A.Cross-references: UNIPARC:UPI000017095C; UNIPARC:UPI0000177AEF; EMBL:X05831
A.Note: the authors translated the codon CCG for residues 51 and 94 as Ala
R.Schwarzbauer, J.E.; Tankun, J.W.; Lemischka, I.R.; Hynes, R.O.
Cell 35, 421-431, 1983
A.Title: Three different fibronectin mRNAs arise by alternative splicing within the cod
A.Reference number: A27252; MUID:84082067; PMID:6317187
A.Accession: A27252
A.Molecule type: RNA
A.Residues: 1586-1720,'T',1722,1813-2477 <SC2>
A.Cross-references: UNIPARC:UPI0000177AF0
R.Odermatt, E.; Tankun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A.Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
A.Reference number: I59049; MUID:86016741; PMID:3863113
A.Accession: I59049
A.Status: translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1722-1810 <RBS>
A.Cross-references: UNIPARC:UPI00000040C; GB:M11750; NID:G204164; PIDN:AAA41170.1; PID
C.Genetics:
A.Introns: 51/1; 94/1; 2416/3; 2454/3
C.Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II rep
C.Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli
F.1-32/Domain: signal sequence #status predicted <SIG>
F.3-3-2477/Product: fibronectin #status predicted <MAT>
F.53-88/Domain: fibronectin type I repeat homology <1F1>
F.98-136/Domain: fibronectin type I repeat homology <1F2>
F.147-180/Domain: fibronectin type I repeat homology <1F3>
F.187-228/Domain: fibronectin type I repeat homology <1F4>
F.232-271/Domain: fibronectin type I repeat homology <1F5>
F.308-342/Domain: fibronectin type I repeat homology <1F6>
F.360-401/Domain: fibronectin type II repeat homology <2F1>
F.420-461/Domain: fibronectin type II repeat homology <2F2>
F.470-508/Domain: fibronectin type I repeat homology <1F7>
F.510-555/Domain: fibronectin type I repeat homology <1F8>
F.561-599/Domain: fibronectin type I repeat homology <1F9>
F.609-692/Domain: fibronectin type III repeat homology <FN3A>
F.718-800/Domain: fibronectin type III repeat homology <FN3B>
F.809-890/Domain: fibronectin type III repeat homology <FN3C>
F.905-987/Domain: fibronectin type III repeat homology <FN3D>
F.995-1076/Domain: fibronectin type III repeat homology <FN3E>
F.1085-1164/Domain: fibronectin type III repeat homology <FN3F>
F.1172-1257/Domain: fibronectin type III repeat homology <FN3G>
F.1265-1348/Domain: fibronectin type III repeat homology <FN3H>
F.1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F.1447-1529/Domain: fibronectin type III repeat homology <FN3J>
F.1537-1619/Domain: fibronectin type III repeat homology <FN3K>
F.1614-1616/Region: cell attachment (R-G-D) motif
F.1631-1713/Domain: fibronectin type III repeat homology <FN3L>
F.1721-1803/Domain: fibronectin type III repeat homology <FN3M>
F.1811-1893/Domain: fibronectin type III repeat homology <FN3N>
F.1903-1984/Domain: fibronectin type III repeat homology <FN3O>
F.1992-2074/Domain: fibronectin type III repeat homology <FN3P>
F.2181-2183/Region: cell attachment (R-G-D) motif
F.2193-2273/Domain: fibronectin type III repeat homology <FN3Q>
F.2296-2375/Domain: fibronectin type I repeat homology <1F10>
F.2341-2378/Domain: fibronectin type I repeat homology <1F11>
F.2385-2420/Domain: fibronectin type I repeat homology <1F12>
F.53-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 232-261, 259-271, 308-335, 333-368, 2366-2378, 2385-2411, 2409-2420/Disulfide bonds: #status predicted
F.2458/Disulfide bonds: interchain (to 2462) #status predicted
F.2462/Disulfide bonds: interchain (to 2458) #status predicted

C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I52257; I65210
R/Vor: H.L.; De Vries, Y.; Hilkens, J.
Biochem. Biophys. Res. Commun. 181, 121-130, 1991
A/Title: The mouse epistatin (Muc1) gene and its promoter. Rapid evolution of the repeat
A/Reference number: I52257; MUID:92068178; PMID:1958179
A/Accession: I52257
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-631 <RES>
A/Cross-references: UNIPROT:Q02496; UNIPARC:UPI000002A11B; GB:M77226; NID:g199835; PIDN:
A/Accession: I65210
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-631 <RES>
A/Cross-references: UNIPARC:UPI000002A11B; GB:M84683; NID:g199842; PIDN:AAA39756.1; PID:
C/Genetic: Muc1
A/Introns: 20/1; 454/3; 472/2; 517/1; 557/3; 607/3

Query Match 3.1%; Score 122; DB 2; Length 631;
Best Local Similarity 21.4%; Pred. No. 1.9;
Matches 122; Conservative 55; Mismatches 207; Indels 186; Gaps 26;

QY 89 RPLFKMTSVGLSGGRLTLRPEKDEATGVDAICTHRDPDTPGDLRQLYLESLT 148
DB 58 RPPGDDTS-SPVSSSTSSPATRAPEDSTAV-LSGSSPATAP-----VNSASSPVA 109
QY 149 HSITELAPYTLDRD--SLVNGFTNRSVPTTSTGVSEEPPTLNNLRVYADMQ 205
DB 110 HGDTSPTATSLSDSNSPVVHSGT--SSAPATAPVDS---TSPVHAGTSSPATSP 163
QY 206 PGSIKFNTNNMKHLSPFORSSLGARTGCRVIALRSVKNCAEFVULLCTYLOPLS 265
DB 164 PGD-----STSPDHSSTSSPATRAPEDSTAV-----LS 194
QY 266 GPGLP-IKOVFHELSQOTGTRGLPYSLDKSLVLYNGVNEP---GDPDEPTPKPAT 319
DB 195 GTSSPATTAAYDSTSSPVADDDTSSPATSLSEBSA-----SSPAHAGTSSPATSPLRDS 249
QY 320 TPLPPLSEATTAMGYHLKT-----LTNFTISNLQYSPDMKGSGATFNSTE 365
DB 250 TSSPVHSSAGI---QNIKTISDLASTPDHNGTSTTTSSALGATSPDHSGTSTTTSSSE 306
QY 366 GVLQHLRLPLFOKSSMGPFLGCOLISLRPEKGAAGVDTCTYHDPVPG-LDIQOL 424
DB 307 SVL--ATTPLY--SSM-PF-----STTKVTSGSAIIPDHGSSVLPRTSSV 346
QY 425 YMELISQTLTGVTOLGFFVLRDLSLFLNGVAPQNLISGEYOINHIWMNLSPNDPTSSR 484
DB 347 LGSATSLVYNTSAIATTPVS-----NGTDP--SVFSQVIV-----SPTMATSS 388
QY 485 YITLLRDIDPKVTLTYKGSQQLHDFRCLVYTNLTMDSVLYVVKALFSSNLDPLSVEQVFL 544
DB 389 HSTI-----ASSSVYSTRVPF-----STFSNSNSPQL----- 414
QY 545 DKTINASPFHMLGSTYQVLVDHVTMESSVYOPTSSSTQHFYLNFTTNLPSYDQKQPG 604
DB 415 --SVGVSPF-----FFLSFYIQNHFNKSLSDPS 440
QY 605 TTYVQMKRNEDALNQLFRN-----SSIK 629
DB 441 SNVYQELKRNISGLFLQIFNGDFLGISIK 470

RESULT 5
S42718
nuclear pore complex protein nup153 - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42718; S37477
R/Morrow, I.; Bastow, R.; Horton, H.; Burke, B.
Biochim. Biophys. Acta 1217, 219-223, 1994

A/Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnuf
A/Reference number: S42718; MUID:94154002; PMID:8110839
A/Accession: S42718
A/Molecule type: mRNA
A/Residues: 1-1475 <MC>
A/Cross-references: UNIPROT:P49790; UNIPARC:UPI000012FC15; EMBL:Z25535; NID:g406224; PII

Query Match 3.1%; Score 121.5; DB 2; Length 1475;
Best Local Similarity 19.4%; Pred. No. 8.1;
Matches 86; Conservative 57; Mismatches 162; Indels 139; Gaps 17;

QY 7 RARRYLFTNRSVSTSTSP-----GTPTYLGASKTPASIFGSAASHLLILFTLNFT 60
DB 351 QAKREKVDQYFPVQRLMTKPKVSIATNRSVYFKPSLTPSG-----EPR 394
QY 61 ITNLR-----YEENMMPGSRKFTTTRVYQGLRPLPKNTSVGLYSGRLTLRPE 112
DB 395 KTNQRIQDKSCGTEYKMTTPGQNR-----DRESGSEYPNFS-----LRA 434
QY 113 KDGATGVDAICTHRDPDTPGDLRQLYLESLTHTSITELGPTLDRDLSLVNGFTNR 172
DB 435 ANGLSSGVG-----CGGMRREHAFVASKPLSEEMVPLPKISLPTS----- 481
QY 173 SSVPT--TSTGVSEEPPTLNT--INNLRVYADMQPGSLKFNTITNNMKHLSPRLQ 227
DB 482 SSLPTNFSSPRTITSSPSPINSQALTKVQMTSPSSGSPWFKFSSPIVKTENAVPE 541
QY 228 RSLGARYTCRVIARSVKNGAETRVLDLCTYLOLSPGGLPLKOVFHELSQOTGTR 287
DB 542 PSSIG--FTFSVPAAKTAELSGSSST-----LEPI-----ISSAHVHT 579
QY 288 L-----GPLY--SLDKSLVLYNGNEPDEP-----PTPKPATPL 322
DB 580 VNSTNCKTPEDCEBPFPAPAILKSGSVLDLKSFGAPKIDSVAAQGTATSPVYTR 639
QY 323 PPLSEATTAMGYHLKTTLNFTISNLQYSPDMKGSGATFNSTGCVLQHLRLPLFOKSSMG 382
DB 640 PAIS-----SFSSSGIGFESLXAGSSWQCDT-----CLLNQKVT 675
QY 383 PFLGCOLISLRPEKGAAGVDT 406
DB 676 NKCIACQAAKLSRDTAKGTGIE 699

RESULT 6
T42977
large tegument protein - ateline herpesvirus 3 (strain 73)
C/Species: ateline herpesvirus 3
A/Variety: strain 73
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T42977
R/Albrecht, U.C.; Fleckenstein, B.
Submitted to the EMBL Data Library, August 1998
A/Description: Primary structure of the herpesvirus atelae genome.
A/Reference number: Z22274
A/Accession: T42977
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2471 <ALB>
A/Cross-references: UNIPROT:Q9YTK3; UNIPARC:UPI000008FC9B; EMBL:AF083424; PIDN:AA095588
A/Experimental source: strain 73

Query Match 3.1%; Score 121.5; DB 2; Length 2471;
Best Local Similarity 18.1%; Pred. No. 19;
Matches 139; Conservative 123; Mismatches 279; Indels 229; Gaps 34;

QY 1 AAQPARARRKTLFTNRSVSTSTSPGTPVYVYASGATSPASIRGSAASHLLILFTLNFT 60
DB 291 SSRKPAQKPKPKSKNSKNTTLTPKHTLI-----EHL-----QDFS 329
QY 61 ITNLRYEENMMPGSRKFTTTRVYQGLRPLPKNTSVGLYSGRLTLRPEKDEATG- 119
DB 330 QSEANKQEHPTFS---HPTER-----KTPGTDSLSGINSKRRKREDDLSNGN 376

QY 120 -----VDAICT-HRPDPTGPGDLREQLYLELSQLTHTSITELEPYTLDRDSLIVY 166
DB 377 VSSKLKEDEDEGWIDDIPTLVNVSPTTEATNSDQETITMGIDENIHDMWSVDODT--DITLDD 434
QY 167 NGFTHRSSVPTTSTGVVSEEPFLNFTINNLRVYAMDMGPGSLKFNITDVMGH--LLSP 224
DB 435 N-FVQJDKVITSLQNIPIINFTPTIIDKPSNRHKGKALHADRILTNIIIEHGLITPS 493
QY 225 LFGRSSLGARYTCGRVIALRSVKNAGT-----RVDLCYLOPLSGEPGPIKOVFHE 277
DB 494 ---PNSMSKCKSLLOFVFLWSEKLSIPTKDLTKTLTNLIITEIAKVASFKL-TNNIF-- 547
QY 278 LSGQTHGTRTGLGSLYLDKSLYLNGVNEBPDEPPTTKPATTFPLPLSATATAMGYHLK 337
DB 548 ---KNNITIKLANK-CHEKIKL-----ETGDN-----YKOLLALISKSTTITQVATT 589
QY 338 TLTNFTTISNLQYSPMGKSGATFNSTEG-----VLQHLRLPLF--QKSMGPFYLG 388
DB 590 EIEELK-NISGM-FTSELGDFSVICTNEBYTALLAIENLKEKIFSRKQELHAEIYFQS 647
QY 389 QLTSLRPEKDGAAATGVDTCTYHPDPVPG-LDIQOLYMWLSQLTGVTQLGFYVLDRDS 447
DB 648 VIITAME-----TFQPIPLPTKYLEIQ-----LEKSK 674
QY 448 LPIINGAPQNLSTIRGEYQIN-----FHIYNNMLSNBDPTSSXYITLLRDIOKATTVLK 501
DB 675 VFLEKLKPEQKLTTE--VNEILLDLHLNKODATEILPV-PDFTTLKNIQSTLQLLH- 730
QY 502 GSQLHDTFRCLVTNLTMDSVLVTKALFSSNLDPSLVEQFLDKTLNLSFHWLGSTYOL 561
DB 731 -----TCYTDLANIDKEVI-----GSTIQ- 748
QY 562 VDIHTEMESVYQPTSSSTQHFYINFTITNLPSQDKAQPGT-----TNYQ 609
DB 749 -----QLSTYGWEVAELSHQWNPSPAPSPILPLQLDELKEITVEQ 787
QY 610 R--NKNIEDALNQLFRNSSIKSYFSDQVSTFRSPVNRHH-----TGVDSLCNFSP 659
DB 788 RYVAKQOQETLNIQIIL--SPVOSILSQAEQSSSTLSPIILOHYITTOAGTVLGBESKNETFES 845
QY 660 LARVDRAVIAIEEFLMTRNGTOLQNFLL--DRSSVLVDGYSPPNNEPL 706
DB 846 LRDVTQKLTSEFLKMLNSTLTLNIQIQIKDISLISNQYMOSETI 895

RESULT 7
F82884
hypothetical protein UH495 (imported) - Ureaplasma urealyticum
C/Spectes: Ureaplasma urealyticum
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #ext_change 20-Aug-2000
C/Accession: F82884
R:Glaas, J.I.; Lefkowitz, E.J.; Glaas, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
submitted to GenBank, February 2000
A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mit
A/Reference number: A82870
A/Accession: F82884
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-5005 <GIA>
A/Cross-references: UNIPARC:UPI0000110214; GB:AE002148; GB:AF222894; NID:G6899495; PIDN:
A/Experimental source: serovar 3; biovar 1
C/Genetics:
A/Gene: UH495
A/Genetic code: SGC3

Query Match 3.1%; Score 121.5; DB 2; Length 5005;
Best Local Similarity 19.6%; Pred. No. 58;
Matches 135; Conservative 108; Mismatches 216; Indels 229; Gaps 39;
QY 136 DREQLYLELSQLTHTSITELEPYTLDRDSLIVNGFTHRSSVPTTSTGVVS-ESEPFLNFTI 194
DB 692 NHEQVY-ELNNSQPOLSEFG-----NELLVNTYNEPNTITDVKTIVLANKVLTILKRS 744

QY 195 N-----NLRYAMDMG-----QPSL-----KENITD-NVMKHLSPLFORSISIGAR 234
DB 745 NLNMEYYLKLKTIIDNNGDVVSDPVSINNVMNNEYENLBDKALK-----SRIYK 795
QY 235 YTGCRVIA-LRNVKNGAETRVLDLCYLOPLSGPGLPIKOVFHELSQTHGTRTGLGPGSL 293
DB 796 FGLVYFKQVNVNITKSANKVM-----NNITPLQIQTA 829
QY 294 DKDSLVLNGVNEBPDEPPTTKPATTFPLPLPS-----EATTMAGHLKTLTLN 342
DB 830 SKINL-----NSPKVTINNITPASADLYPLVSTDDIPAKDQVIDVTIGNKNTKN-DLM 883
QY 343 FTISNLQYSPDMGKSGATFNSTEGVLOHL--LRP-----LFQKSMGPFYLGQOL 390
DB 884 FT-SNLEVD-DITK-----TWGVKIHANNLSPEVNYQIKSVKFRQKFLGAFVNV-- 931
QY 391 ISLRPEKDGAAATGVDTCTYHPDPVPGGLDIOQLYMWLSQLT-----HGVTOLGFFYVL 443
DB 932 ---NSDMNHLIDSQKT-----PGSTFKASFDLVSVTASDVVDANVNTNSVHIV 979
QY 444 DRDSLIFNGVADPQNLSTIRGEYQI--NPHIVNMNLSNP----- 479
DB 980 NNDGTSINACKAKIYNDGEHDLVSNPFVLNVGVNEYPNLDLKGRIYGFKLIYTE 1039
QY 480 PTSSSEY-ITLLDIDQKATTVLKSGQLHDTFRCLVTNLTMDSVLVTKALFSSNL----- 534
DB 1040 PQNDYKFSFLNN--QKITNFKTASVNE-----QLTIDTKLRKP--DSNLKIN 1086
QY 535 -----DP-----SLVEQFLDKTLNLSFHWLG-----STYQOLVDIHTEMESVYQ 575
DB 1087 LKQLINDPNDPFLQDSILEITHEDEKDKTHNAVIGKINVDANNKTLBESVENTTFFKIQ 1146
QY 576 PTSSSTQHFYINFTITNLPSY-SQDKAQPGT--NYQRNKNIEDALNQLFRNSSIKSYFS 633
DB 1147 P-----NHKYL--VDNINVTAKNKIQPANNISNNSKNGSIYDAS--NPSKILSFYN 1194
QY 634 DCQVSTFR-SVPRRHHTGVDSLCSNPSPLR-----RVDRAVIAIEEFLMTRNGTOLQNF 687
DB 1195 EIFVNNINNOFP-----TNLNPASIDVELKSQNLKDYLRALYIDNNHOKIW 1245
QY 688 LDRSSVLVDGYSPPNNEPLTGNADIQH 715
DB 1246 SDYASY-----NNVDLAH 1258

RESULT 8
T41144
hypothetical serine rich protein - fission yeast (Schizosaccharomyces pombe)
C/Spectes: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
C/Accession: T41144; T41591
R:Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A/Reference number: Z21973
A/Accession: T41144
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1131 <HIL>
A/Cross-references: UNIPROT:O74851; UNIPARC:UPI000006A713; EMBL:AL031907; NID:G3766362;
A/Experimental source: strain 972h-; cosmid c18
R:Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z21968
A/Accession: T41591
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 44-1131 <MUR>
A/Cross-references: UNIPARC:UPI0000161F34; EMBL:AL031543; NID:G4239667; PIDN:CAA20837.1
A/Experimental source: strain 972h-; cosmid C74
C/Comment: For a possible alternative initiator product, see PIR:T42367.
C/Genetics:
A/Gene: SPC74.07C; SPDB:SPCC18.01C

A:Map position: 3
C:Keywords: alternative initiators

Query Match 3.1%; Score 121; DB 2; Length 1131;

Best Local Similarity 18.6%; Pred. No. 5.7;

Matches 161; Conservative 130; Mismatches 353; Indels 222; Gaps 30;

```

QY 2 ACPARRARTKLFTRSSVSTSTPTPTVYLGASKTSPASIGPSAASHLLILFTLNFT 61
DB 341 AASSSSASATATASASSIAT--SPTTSSNNVSSISTSSMSAVSVISVQSSIASIT 398
QY 62 TNLRYEENMPPGSRKRENTTERVLOGLRPLFKNTSVGPVYSGCRLTLRPEKGEATVD 121
DB 399 S-----NAYIATSKGLNSGVSTLLASPTSSSTFVTSI-----LRSSIDGASASS 445
QY 122 ---AICTRPDPPTGPRDLREQLYELISQTHSITEGPTTLDRDSLIVNGFTHRSVPT 178
DB 446 ASLAVPTVSSSTTG-----SLHYK-TTTTWTVEVFTRYLDDSTPTVS---SSIFST 494
QY 179 ST-----GVSEBPFTLNFTLNLRVYADMQPSLKNITDNVKKHLASPLFQR 228
DB 495 ATEADTSTVQTSATIDSSSTSNIGSSSVYASSTGALSNSLSSTSSVSTIYPNAS 554
QY 229 SSIGARATGCRYIALRSYKNGAETRVDLLCTYLQPLSGPLPKOYFHELSCQTHGITEL 288
DB 555 SVYASSTALSSNSLSSTSSAST-----SVIPLASSYEVASNSDYYQTVSITAS 608
QY 289 GPYSLDKDL-----YLANG-----YNEGPPEPTTPKPAITPLPLSEATTMAG 333
DB 609 GTTSTSTSEIVSTPASNSNTGSLNGTSSFFVNSGVPSQTTPTSSSITGSSQSLKETSP 668
QY 334 YHLKTLTLNFTLSNLQYSPDMKGATENS-----TEGVLDH 370
DB 669 AVVSS-TVSYTSSVD-----SSSTVNSTGSSSDSGSFSGTYSDDTTITTSVSSI 720
QY 371 LRLPLFOKSMGPFYLCQLISLRPEKDEATGVDITCTYHDPVPGGLDIQOLYWELSQ 430
DB 721 LSSPTSMOSVS-----RPGSGDASGFNT-----IFRSIQ 752
QY 431 LTHGVTQLCPYVLDRLSLFINGAPONLSIRGEYQINFIIV-----NMNLSNP 478
DB 753 SSGDET--SGYITSSNSNSONSASEPOTAFSSSSSATPTTOSISITSVSSOSNMSSYS 810
QY 479 DPTSSSYITLLRDIDQKV-----TTLKSGQLDHTPFPCV 514
DB 811 SPLSSNSVSTSIISISIASSTSTSPSISIASFFDASGFTSITNGKAGSSSFALA 870
QY 515 TNLTDSVLVTVKALPSSNLDPSLVEQVFLDKTLN-----ASFHMLASTYQLDVI 564
DB 871 SNSBSGA-----SDVLSTIAKPTFKPSTNSNGSTSYSPSSSSNEGTTYSNI 921
QY 565 HTTMESSVYQP--TSSSTOHFYLNFTTNLFYSQDKAOPGTTNYQNRKNITEDALNOL 622
DB 922 TVT---SSTLKPSLTSSVSTASISASASNTLS---TEPKTFS---SSSTLSBSISSI 972
QY 623 FRN-----SSIKYFSDCOVSTFRSVN--RHHTGVSLCNFPLAR-----663
DB 973 NTNSLTIVKCBSSLSSTTSGLTSSSTIIPSTRSBNSSBSASGKSSSSTSLVQSN 1032
QY 664 -VDRVAIYERF-----LMTNRGTQLQNFLLDRSSVLVGVSPNNEPLTGN-----710
DB 1033 PVKTVVSLSSYKTKTSKISLVKPKTYVTVDVETNVVVQTHVSVYEHSTSTVHTTL 1092
QY 711 ---ADIQHSQGRSSLEGPREFQLIS 733
DB 1093 YEVADVEASTKTSRPSAKSKRAVVS 1118

```

RESULT 9
T34235
hypothetical protein F22A3.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T34235
R:Halloworth, K.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans coemid F22A3.

A:Reference number: 221492

A:Accession: T34235

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-532 <HAL>

A:Cross-references: UNIPROT:Q19695; UNIPARC:UPI000017B91C; EMBL:U41547; PDB:AAA83194.1;

C:Genetic:

A:Gene: CESP:F22A3.1

A:Introns: 55/1; 71/1; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 331/3; 357/1; 391/1; 511

F:446-527/Domain: etc DNA-binding domain homology <ETS>

Query Match 3.0%; Score 118; DB 2; Length 532;

Best Local Similarity 20.5%; Pred. No. 2.7; Indels 162; Gaps 25;

Matches 101; Conservative 59; Mismatches 171;

```

QY 255 DLLC-TYLOPLSG-----PGLPIKQVFEHLSQOQTHGITRLGPYSLDKDSLILYNGYNEP 306
DB 9 DFLCTGMSVSGIKKQASPGISRESVFGAKRCAVAARAP-----52
QY 307 GPDPEPTTPKPAITPLPLSEATTMAGYHLKTLTN---FTISNLQYSPDMKG--SATF 361
DB 53 -PEEPFPPTPTLLFKLSERO---FH---GLNPAFPENMLEYKXGCKSDSSSM 103
QY 362 NSTEVLQHLRPL-----FOKSMGPFYLCQLISLRPEKGEATGVD 406
DB 104 NGT-GSVGRNLSLPEPHSGTSTASPPFVSEF-PF-----DDLPGLDQ 148
QY 407 TCTYAPDPVGP--GHDIOOLYWELSQLTHGVTQLGFYVLDRL-SLFINGYAPQNLISGE 463
DB 149 VANNVPHEDMCNLPIDPIENNR-----FSGDADHSFTVKNKIEINI-----192
QY 464 VOINFIHVMNLSNDPTSSSEYITLLRD-----IQDKVTLYKGSQQLDHF-----509
DB 193 --LNFN-VNPEIAQNGDLTDQIDYRDLRLHLIDISTCAKGLPDPFYLMSSEHQA 249
QY 510 -----RFLCVTLN-----TMSVLYTVKALPSSND 535
DB 250 RMINEMCMQFNLOPPRNCISITGIDLGMSQKDEMLPAGGDTLHAQLQVMTAEVNYHP 309
QY 536 PELVE---QVFLDKTLNLSFHWLGST-YQVLDIHTEMESSVY-----OPTSSSSTOHF 585
DB 310 PTVQSSGCTAENNMGSCTNMLASTNNQTNMAAENHNHFFNGNGYPMMSMS--F 367
QY 586 YLNFITITMLPYEQDKAOPGTTNYQNRKNITEDALNQLFRNSSIKSYFSDCOVSTRSVN 645
DB 368 FQGGTVLPSPNSDTSNSNSQ-DNMDDDDIDLMNN-----SNCGFSNPFHNOG 415
QY 646 RHHTGVDSLGNFS 658
DB 416 YNMSPIDAMNGS 428

```

RESULT 10

DNA-binding protein cl (D) - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: A38926; A38917; S12122; S12769

R:Sluareakti, D.

submitted to GenBank, October 1990

A:Reference number: A38926

A:Accession: A38926

A:Molecule type: mRNA

A:Residues: 1-1377 <SLU>

A:Cross-references: UNIPROT:P19538; UNIPARC:UPI000016BA41; GB:X54360; NID:g7732; PID:g77

R:Orenic, T.V.; Sluareakti, D.C.; Kroil, K.L.; Holmgren, R.A.

Genes Dev. 4, 1053-1067, 1990

A>Title: Cloning and characterization of the segment polarity gene Cubitus interruptus 4

A:Reference number: A35817; MUID:90346286; PMID:2166702

A:Accession: A35817
A:Molecule type: mRNA
A:Residues: 1145-1151, 'K', 1152-1377 <ORE>
A:Cross-references: UNIPARC:UPI000017BE89; GB:X54360
C:Genetics:
A:Gene: FlyBase:cl
A:Cross-references: FlyBase:FBgn0004859
C:Keywords: DNA binding; zinc finger

Query Match 3.0%; Score 117.5; DB 2; Length 1377;
Best Local Similarity 19.6%; Pred. No. 14;
Matches 132; Conservative 83; Mismatches 224; Indels 233; Gaps 31;

QY 166 VNGFTHRSSVPTSTGVSEEPFTLNFTNN-----LRTMAMGQSGSL 209
DB 675 VNGVRASDLSLTSPDDLAE-----NINLDDGMNCDVDVADLPVLRMVMVINGNAN 729
QY 210 KFNITDVMHGLSLPLFORSSLGARYGCRVIALRSYKNGAETRVLDLCTYLOPLSGPL 269
DB 730 ASTIGSVLAR-----QRRFG-----RLDTKGINSSTIMLCNIPF----- 764
QY 270 PIKQVHELSQQTHGTRIGPYSIDKDSLNGYNEBGPDEPTTPKPAATFLPPLSEAT 329
DB 765 -----SNRTFGISELNQRI TELKM-----EBGTDAEIKIPKLPTTIGGISEDP 808
QY 330 TAMGYHAKTLTLNFTISNLQYSPDMKGSATFNSTEGVLDHLRLPFOKSMGPFTYLGQ 389
DB 809 LQ-----NOTSFNNTVSNKQ-----GVSSSIGQOPRRDSQNSTASTYGGSMQ 851
QY 390 LISLRPEKDGATGVDP-----TCTYPRPVGGLDIOQLYMWELSQLTHG----- 434
DB 852 ---SRSSQSQVSIFTPMRNPGSCNSTASY-DPISGCSRRS-----SQMSNGANCSF 903
QY 435 VTQGFVYLDKDS-----LFINGYAPQNLIRGEYOQINFIHVMNLSNPDPTSEYI-TL 488
DB 904 TSTSGLPVLNKESKSLNACIN---KENIGVQG-----VGIYNSLPPPPSHILATN 953
QY 489 LRIOQDKVTLLYKSGQ-----504
DB 954 LKRLQKRDSEYHNFSGSRFVSPYSMSLHKKNKPVGENEFDAISNARQDTPVNPIN 1013
QY 505 ---LHDPFRCV-----TNLTMSVLTVVKALFSSNLDPSLVEQ 541
DB 1014 LDELITNISRSTTPHSDIVNGKTNINASLKNONLAKDLFTYSIKADAMATSDQHPNER 1073
QY 542 VFPLDKT-----LNASFMLGTYQVLDI--HYTE-MESSYQPTSSSTQ 583
DB 1074 INLDEVABELLPDEMQLYNLVMKDDTNHLEKHOAVPVGSNVSEPTIASNHYRQSNL--- 1130
QY 584 HFTLNFITTNLPYSQDKAQPGTTNYQNKKNIEDALNQLFRNSISIKYSPDCOVSTFRSV 643
DB 1131 -YTNKQILTPPSNVD-IQNTTFTVQDK-----FAMTAVGGSFQRELSLT-AV 1177
QY 644 PNHH-HTGVSLCNFSPLARRVD-----RVAIYEELRMTNRNGTQLONFTLDS-----S 692
DB 1178 PNHHGAKKCSFHHSQSKYNTDIGSKQGSALPSAHOKREKSN--YNOIIDSMTSLPE 1235
QY 693 VLVGVSPNENE 704
DB 1236 LNVDSITYP-RNE 1246

RESULT 11
A44140
cellulose-binding protein A precursor - Clostridium cellulovorans
C:Species: Clostridium cellulovorans
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44140
R:Shoseyov, O.; Takagi, M.; Goldstein, M.A.; Doi, R.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3483-3487, 1992
A:Title: Primary sequence analysis of Clostridium cellulovorans cellulose binding protein
A:Reference number: A44140; MUID:92228810; PMID:1565642
A:Accession: A44140

A>Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-1848 <SHO>
A:Cross-references: UNIPROT:P38058; UNIPARC:UPI00001271G5; GB:M73817; MID:g144748; PIDN
C:Genetics:
A:Gene: cbpa

Query Match 2.9%; Score 116; DB 2; Length 1848;
Best Local Similarity 17.7%; Pred. No. 28;
Matches 133; Conservative 92; Mismatches 244; Indels 284; Gaps 30;

QY 14 FTHRSSVSTSTSPGPTV-----YLGASK-----TPASIFGPSA-----S 49
DB 154 YQTNINYSDDASSSTVVPKVTGIGAKVIGTARGPVPSIINPTSATPDKNVTYKQA 213
QY 50 HLLILFTLN---FTTNLRYEENMPPGSRKNTTFRVLQ---LRLPFRKTSVGPY 101
DB 214 DVKTMTTLNGNTEFKITTDAN-----GTALNASTSVSGNDVTISKAYLAKOSVGT 266
QY 102 SGCRLLTLNPEK-----DGEATGVDAICTHRPDPGPGLDRE 138
DB 267 LNFNFSAGNPQKLVITVVDTPVEAVTATIGKQVNAGETVAVFVNLTKVP---AAGIATI 323
QY 139 QLYELSQLTHSITE-----LGPYTLDRDSL-- 165
DB 324 ELPLTSDASLEVVSTIAGDIVLNPSVNSSTVSSGTYKLLFLDPTLGSQILKDGVPAT 383
QY 166 -----VNGFTHR-SSVPTTSTGV---SEEPFTLNFTNNLRVMADMGPQSGSLKEN 212
DB 384 IFPKAKAIGTAKVTSVLAAGPVPVGAQOLDEKPCAVN-----PGVTTIN 429
QY 213 ITDNNKHLISLPQSSISGARTGCRVIALNSYK---GAETRVLDLCTYLOPLS--- 285
DB 430 PIDNRQOISVG---TATYKAGEIAVAVPVLTVSPSTGATGAEOYSPATLLEVASVTA 485
QY 266 -----GP-----GLPIKQVHELSQOQTHGITLGPYSIDKDSLNGYNEBGPDEP 311
DB 486 GDIVLNPTNPFSTVGNVYKILFLD-----DPLGSQILSKDGVPT-INPKAKAVT 536
QY 312 PTPKPAATFLPPLSEATTAMGYHAKTLTLNFTISNLQYSPDMKGSATFNSTEGVLDL 371
DB 537 SFVTTFTVTVSGRVPFADGLTAEVQSKT-----AAGSVTINIDPILPEPT 580
QY 372 LKPL---FOKSSMGPFYLGCOLISLRPEKDGATGVTCTYHPDPVVGGLDIOQLYMWEL 428
DB 581 ISPVATTFPKK-----APADATMT-- 601
QY 429 SQLTHGVTQGFVYLDKSLFINGYAPQNLIS--IRGEYOQINFIY----- 471
DB 602 -----LNGYTFNGITGLTSDYISGNVVKLSQAYTLAKQVGLD 640
QY 472 ---NMNLSNPDPT-SSSEYTLRLDIDQKVT-----TLYKG-----SQL 505
DB 641 TLTFNFSNKNKATATLAVSINDAPKTVTATVGTATVAGTAVVAVPVTLNSVGSITABL 700
QY 506 HDTFEFL---VTNLMDSVLTVVKALFSSNLDPSLVEQVFLDKTLNASTHMLGTYQVLD 563
DB 701 QLSFDATLLEVASITAGDIVLNPSVNFSSVNGSTIKLFLDPTLGSQILSKDGVPAITN 760
QY 564 IHTMESSYQPTSSSTQHFLNFTINLPY 596
DB 761 FPAKSVSTVTTTPVKVSGTPVF-ADGTLAELSY 792

RESULT 12
F69009
probable membrane protein MTH1074 - Methanobacterium thermoautotrophicum (strain Delta)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: F69009
R:Smith, D.R.; Douchette-Stamm, L.A.; DeJonghe, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Oiu, D.; Spadeford, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N
ki, S.; Church, G.M.; Daniele, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct
A:Reference numbers: A69000; MUID:98037514; PMID:9371463
A:Accession: F69009
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1474 <MTH>
A:Cross-references: UNIPROT:Q27146; UNIPARC:UPI0000666BF; GB:AE000878; GB:AE000666; NID
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1074
C:Keywords: duplication

Query Match 2.9%; Score 115.5; DB 2; Length 1474;
Best Local Similarity 20.5%; Pred. No. 21;
Matches 158; Conservative 92; Mismatches 306; Indels 215; Gaps 38;

QY 26 PGTPT-VYLGASTPSPASIFGSPASASHLLILFTLN-FTITNRYEENMMWGSRRKFTTERV 83
DB 393 PNNATGVYVTDLLPQLSFSVASASRGVNSTGMITGNLEVFETV-----TLNITATV 447
QY 84 LQGLRLPLFKMTSVGLVSGCRLT--LLRPEKDEATGVDAICTHRPDTGRLDREQLY 141
DB 448 -----TATGAIYNNANVTGDFPDM--ANNYASALNPPASDLTIDK---- 489
QY 142 LELSLQTHSITELGFTLDRDSLXYNGFTHRSVPTTSGVSEEPF----- 188
DB 490 -----SVNNRPEI-VGENIOTYITVSNG--PNNAGVVEVDLPAGLIPISATPEK 538
QY 189 -----TLNF-TINNLRVADMGQPSGLK-FNITDVMKHLPLP--QRSS 230
DB 539 GSYGWTGMYVNTLNLEIALTLTIARVNATGSLTNFANIT-----SPNFDPNDNN 590
QY 231 LGARVYGCRIALRSYNGAEFTVD-----LICTYIQLSPGLPIKOVHE-LSQO 281
DB 591 DTAENVGIPVADLLIKQVSDPRPDYGVVFTVAVTNIGPSNATVATDILSPGLVYL 650
QY 282 TGGITRLGPSLIDKSLYNGVNEPQDEPPTPKPATFTPLPPLSEATTAMGYHLKTLT 341
DB 651 SHRVTO-GTYNATGWTGYGALNY-----AASALMLVLYLVNTGDSNNTV-- 695
QY 342 NPTISNLQYSPDMKGSA--TFNSTEGLVLOHLRPLFOKSSMGPFYLGQQLISLRPEKDQ 399
DB 696 --SVTGENRDPDRITNNDVASTLNAVSADLS-----IQKTVD-----REVINN 735
QY 400 AATGVDTTCTYHPDPVPGGLDI--QQLYELSQLTGTGVLQGFY---VLDRDSLFTNG 453
DB 736 GRTATFTVVRNAGPPTPSNVVSDLLPAGLSIISYTVTQGSFNTTGVMEVGLPALPQ 795
QY 454 APQNLISIRGE--YOINPHIVMNLSPDPTSEYITLL-----RDIQDKVTLLYKGS 503
DB 796 ATTLTVARATQAGFQTN--LVNVSSELPPDLPGDNDAVTVDRPADVKITTVNTAP 853
QY 504 QLHDTFRFCL-VTNLTMDSVLVTVKALFSSNLDPISLVEQVFLDKTLNASEPHMLGSTYOLV 562
DB 854 DPEDTVVFYITVNLGPDATV-----RT----- 878
QY 563 DIHVTMESSVVOPTSSSTQHFYLANFTITNLEPYSDKAOPGTTNQRKRNIEDALNQL 622
DB 879 ---VDTMPGQLVYQSHSASAGIYFEPNV---WTYDSIAPGASE-TLNTTVLVNATGCM 930
QY 623 FRNSISKYSFSDCOVTFRSPRHHHTGVDSLGNFSLPARRVRAVIAIEEFLMTNGNQ 682
DB 931 INTVASTSTTEYDDLT-----NNHAG--LNN---AEAVADIAVKVLTLPINNGQ 977
QY 683 LQNFLLDRSSVLVDGYSPNRNEPLTGNAD-----IQHSGGRSSLEG 724
DB 978 ITNFT-----VYTNNGPN---DATGAVTDILPPLGLSLSHASQCTFAG 1020

RESULT 13
A54280
cell differentiation protein lagc precursor - slime mold (*Dictyostelium discoideum*)

N:Alternate names: loose aggregate C
C:Species: *Dictyostelium discoideum*
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A54280
R:Idynes, J.L.; Clark, A.M.; Shaulsky, G.; Kupea, A.; Loomis, W.F.; Firtel, R.A.
Genes Dev. 8, 948-958, 1994
A:Title: lagc is required for cell-cell interactions that are essential for cell-type di
A:Reference number: A54280; MUID:95011593; PMID:7926779
A:Accession: A54280
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-888 <DYN>
A:Cross-references: UNIPROT:P42523; UNIPARC:UPI000012E1FF; GB:U09478; NID:6495172; PIDN:
A:Note: authors translated the codon TCA for residue 34 as leu
C:Genetics:
A:Gene: lagc
C:Superfamily: *Dictyostelium discoideum* cell differentiation protein lagc
C:Keywords: transmembrane protein

Query Match 2.9%; Score 115; DB 2; Length 888;
Best Local Similarity 19.6%; Pred. No. 10;
Matches 157; Conservative 109; Mismatches 235; Indels 298; Gaps 47;

QY 110 RPEKGE--ATG-----VDAICTHRP-----DPT-----GPGLD 136
DB 130 KPKTSGEDIVTGSYLRLFGGNPLNSIDVKNFSDPFDCCNITVTFPPGSG 189
QY 137 RQQLYELSQLHSTELG---PYTLD-----RSLVNG--PTHRSSVPT 177
DB 190 KRLLYD-----ETGDNFVPSYESPIISSVSQSKITITNGDNFTDXDLVY 240
QY 178 TSTGVSEEPFLNFTI-----NNLRVADMGQPSGLFNIT-- 214
DB 241 SFQGI--DQP--NFIISVNHQIQVNNYNR--DEPMSVNTIYVEVSEIKOVYHCF 291
QY 215 -----DNVKKL-----LSPLFOKSSIGARYTCGVIALRSVKNQ 249
DB 292 PAITISISVSNHLDGIVTIKEKSLTNLYLTPESI--TIGDYK-----VLIISTTE 343
QY 250 AETRYDLCTYIQLSPGLPIKOVFH-----ELSQOTHGI----- 285
DB 344 LBECKLD--ANELGGKXLPVNVNFGGCDSTSPNGVSTYVNIPTLSRGSYSNGIVTLIG 398
QY 286 TELGPSYLDKSLYNG--YNERGPDEPPTPKPATFTPLPPLSEAT--TAM 332
DB 399 TNLGTMNESSIDLXGDDIKNTNISQPNVSSSB-----KSYFELPHLRGRFNINFRS 453
QY 333 GYHLKTLTINFTIS-NLQYSPMGKGSATFNSTEGVLQHLRPLFOKSSMGPFYLGQQL 391
DB 454 GITAKTLISASLSVNVINRPTV-----SNGIL-----NIEIYMDCTIS 493
QY 392 SLRPE-----KQGAATGVDTCTYHPDPVPGGLDIQQLYELSQLTHGVNQ 437
DB 494 SSAPSIYVGDSSSASPCSPSSNSYETTC--PPYGTGIN-KQIFKLNSET-- 544
QY 438 LGFVYVLDKSLFLINGAP--ONLSIRGE--YOINPHIVMNLSPDPTSEY 485
DB 545 -----VSDQSS-----YAPPEVENRTISDGTNIEHGNFGASTLKYLLNGSDISSR 594
QY 486 ITLLRDID--KVTTLYK-----GSQLHDTFRFCL--VTNLTMDSV-- 522
DB 595 ---IQLELDHQTLIKLDSYENGPNITVDGVNMOSLFYLTLPVLYRITNDKNKTLAC 651
QY 523 -LVTVKALFSSNLDPISLVEQVFLDKTLNASEPHMLGSTYOLVNIHTEMSSVVOPT 577
DB 652 GIIYVS--GKQLLISDKFKNVNSNNKNTTVFAODEKILLVRDESRSSSLPVTTFICV 708
QY 578 -SSSTQHFYLANFTITNLEPYSDKAOPGTTNQRKRNIEDALNQLFRNSISKYSF 633
DB 709 RSGPSTLLTYIKPMISEITIKIEKGLAIIRG-YSTFDILNASLTVSSSEVPISCL 767
QY 634 DCQVS-----TFRSVNRHHTGVDSL-CNPSPLARRVRAVIAIEEFLMRNQTOLQ 684

Db 768 ECSLSPNEILDDSDSETINTNSNTDCLSCHSGSSVKNISGV-----LYLNFNSTFOY 821
QY 685 NPTLDRSSVLVDGVSPPRN 703
Db 822 NVTIEIKT-----SPSPN 835

RESULT 14

A35364
carcinoembryonic antigen-related protein (clone rncGM1) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 09-Jul-2004
C/Accession: A35364
R/Rebstock: S.; Lucas, K.; Thompson, J.A.; Zimmermann, W.
J. Biol. Chem. 265, 7872-7879, 1990
A/Title: CDNA and gene analyses imply a novel structure for a rat carcinoembryonic antigen
A/Reference number: A35364; MUID:90243655; PMID:2335509
A/Accession: A35364
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-709 <REB>
A/Cross-references: UNIPROT:Q63111; UNIPARC:UPI0000E81AF; GB:M32474; NID:G203430; PIDN:
C/Superfamily: carcinoembryonic antigen-related protein rncGM1; carcinoembryonic antigen
F/1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F/168-217/Domain: immunoglobulin homology <IMM1>
F/242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>
F/480-612/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>
F/633-690/Domain: immunoglobulin homology <IMM2>

Query Match 2.9%; Score 114.5; DB 2; Length 709;
Best Local Similarity 20.0%; Pred. No. 7.6;
Matches 136; Conservative 80; Mismatches 263; Indels 201; Gaps 30;
QY 134 GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTSTGVSEBPTLNT 193
Db 70 GLTMSGLVALYSLTAVVTGVPVHSGRETLTSGSLMIGNVQKDTGFTY----- 120
QY 194 INNLRYADMGQGSGLKFNITDVMKGLSPFORSSLGARYTGCRVIALRSVNGAETR 253
Db 121 --LRTISNMG-----IVSNTSLH-LHVFSTLLCGRAATSQA--LSIESVPTSISK 168
QY 254 VDLICTYLOPLSGPLP--IKOVFH-----ELSQOHTGITRL--GPTSLDKDSLY 299
Db 169 ESKL-----LHANLPENIRAIFWYKGAIVFKDLEVARIVITGNSSVPPPAHSGRTMY 222
QY 300 LNC-----YNEGPDEPTTPKPAITFLPPLSEATTAMGY-HLKTLLNFTISLQYSPDM 354
Db 223 SNCSLLQNTVTRNDAGYTLKTLST-----DKTEIAVYQLOVDTCFMSYAGPPISAQL 276
QY 355 GKGSATFNSTEG---VLQHLRP-----LFQKSMGPFYLGCOLISLRPEKD 398
Db 277 TVESAPTSVAEGASVLLVLANLPENIRAIFWYKGVILFKDLEVARIVITGNSSVGLPAHS 336
QY 399 GAATGVDTTCTHPDPVGPGLDNLQOLYWEISQLTHGTC--LGPVYLDRLSLINGAPQ 456
Db 337 GRFT-----MWSNGLLQNTVTRNDAGYTLRTSLDIAKAV-- 373
QY 457 NLSIRGEVQINFIIVNNILSNPDTSEYITLLRDIODKYTT-LYKSSQLADTFERFLVY 515
Db 374 ---VHQQLQVN-----TSSCCDPLTPALLTI-----DVPRIHAKG----- 406
QY 516 NLTMDSVLTVKALFSSNLDPSLVEOVFLDKTLNASTFHWLGSTYQVLDIVHTEMES-- 572
Db 407 ---ESVLLQVR-----NLPEDL-----RMFIWPKSVYTSQIFKIAEVSRAIN 446
QY 573 VYQPTSSSTQHYLNFTINLPYSODKAPGTTNVRNKRNIEDALNQLFRSSISKSYF 632
Db 447 VFGPAPASGREYVYTNGL---LLODATEKDTGLY-----TLQIYYRNFKLETAAH 493
QY 633 SDCQVST-----FRSVPRHHTGVDSLGNFSLPARRVRAVAYEEFLRMTEGRT 681
Db 494 VQVSVHTCVAPSTTGQLVISVSPNVVGGDVL-----LLVHNMP 534

QY 682 QLQNFPLDRSSVLVDGVSPPRNPEPLTGNAGDI--CHSGRSSLEGPREFEOKLISEEDLNM 739
Db 535 NLQSFMYKGVAILVNHHEISRN-IISNRSTLGPAPASGREYITSGNSGLLHNATEEDNGL 593
QY 740 HT-----GHHHHH 748
Db 594 YTLMTVNRHSETQGIHVH 613

RESULT 15

T07015
Cf-4A protein - tomato
C/Species: Lycopersicon esculentum (tomato)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T07015
R/Takken, F.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
Plant J. 14, 401-411, 1998
A/Title: Identification and De-tagged isolation of a new gene at the Cf-4 locus of toma
A/Reference number: Z15863; MUID:98335213; PMID:9670557
A/Accession: T07015
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-855 <TAK>
A/Cross-references: UNIPROT:O50024; UNIPARC:UPI00009FC28; EMBL:Y12640; NID:e1289424; P
C/Genetics:
A/Experimental source: strain Cf-4; isolate MM-Cf-4
A/Map position: 1

Query Match 2.9%; Score 113.5; DB 2; Length 855;
Best Local Similarity 19.6%; Pred. No. 12;
Matches 149; Conservative 111; Mismatches 209; Indels 293; Gaps 43;
QY 54 LFTLNFTINLRYEEN-----MWPGRKNTTERRVLA-----GLRPLPKNTS 96
Db 42 MFTINPMASNYCYDRRTLLSMNKSTSCSMDGVHCDETTGQVLELDGCSQLQCKFHSNNS 101
QY 97 VGPVYSGCULLTLRPKDEAGVDAICTHRDPPTGPGLDREQLYLELSQTHSITELGP 156
Db 102 LFOGLSLKRLDL-----SSNDFTG-----SPISP-----KFGESFDLTH----- 135
QY 157 YTLTD-RDSLTVNGFTHRSSVPTTSTGVSEB-----PFTLNFTI 194
Db 136 --LDLSDSNF-----TGVIPEISHLASKLAVLRISDYKSLGHNBEILL 179
QY 195 NNILRYADMG-OPGSLKFNITDVMKGLSPFORSSLGARYTGCRVIALRSVNGAETR 253
Db 180 KNLQTLRELHLESVNISITIPSNFSFHL-----TNLRSLSTELR----- 218
QY 254 VDLICTYLOPLSGPLPIKOVFH---ELSQOHTG---ITRLGPHYSLDKDS---LYLNG 302
Db 219 -----GVLPRVFHLSNLELDLSYNQLOLVTRPPTTIWNSASALVKLYLSR 264
QY 303 YNEGP--PDEPTTPKPAITFLPPLSEA-----TLANGYHLKTLNFTISNLQYSPDMGK 356
Db 265 VNAGNIPD-----SPSYLALHEDLMVTNLSGPIPKPL--WNLTNLE-SLDL-- 310
QY 357 GSATFNSTEGVLOHLRPLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTYHDPVYG 416
Db 311 ---DVNHLGPIPOL--PIFEK-----LNSL-----TLGNND 339
QY 417 PGDLIDQOLYWEISQLTHGVTQLGFFVYLDRLSLFINGVAPONIS---INGEY---QINF 468
Db 340 GGLLEFLSPFRSMTQLEE-----LDPSNSNLTCPIPSNVSGLRNLQSLYLSNNLNG 390
QY 469 HYNM-----NLSNPPTSSEYITLLRDIODKYTTL--YKGSOL-----HDTFRP 511
Db 391 STPSWLFPLDPLSLRSLDLSNNTPSGKIQEFKSTLSLVITLKQNDLKKGPINSLNQSLOP 450
QY 512 CLVT--NLV--MDSVLTVKALF-----SSNLDPSLVEOV-----LDKRT 547
Db 451 LLLSHNINIGHSSISCNLKMVLVDLGSNNLEGTIPQCVVERNEYLSHLDSNNRLSGT 510

